

09/084,471
original

SEQUENCE LISTING

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(1) GENERAL INFORMATION

(i) APPLICANT: Murphy, Patricia
White, Marga
Rabin, Mark
Olson, Sheri
Yoshikawa, Matthew
Jackson, Geoffrey
Eskanderi, Tara
Schryer, Brenda
Park, Michael

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(ii) TITLE OF THE INVENTION: NOVEL CODING SEQUENCE HAPLOTYPES
OF THE HUMAN BRCA2 GENE

(iii) NUMBER OF SEQUENCES: 111

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Howrey & Simon
(B) STREET: 1299 Pennsylvania Avenue N.W.
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20004

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

40

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

45

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Halluin, Albert P
(B) REGISTRATION NUMBER: 25,227
(C) REFERENCE/DOCKET NUMBER: 5371.31.US02

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-463-8109
(B) TELEFAX: 650-463-8400
(C) TELEX:

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(2) INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

09084471.052998

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: exon
(B) LOCATION: 1...50
(D) OTHER INFORMATION: Exon 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15 TCCTGTTGTT CTACAATGTA CACATGTAAC ACCACAAAGA GATAAGTCAG

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: exon
(B) LOCATION: 1...182
(D) OTHER INFORMATION: Exon 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

35 ATTTAATTAC AAGTCTTCAG AATGCCAGAG ATATACAGGA TATGCGAATT AAGAAGAAAC 60
AAAGGCAACG CGTCTTTCCA CAGCCAGGCA GTCTGTATCT TGCAAAAACA TCCACTCTGC 120
CTCGAATCTC TCTGAAAGCA GCAGTAGGAG GCCAAGTTCC CTCTGCGTGT TCTCATAAAC 180
AG 182

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: exon
(B) LOCATION: 1...188
(D) OTHER INFORMATION: Exon 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

55 CTGTATACGT ATGGCGTTTC TAAACATTGC ATAAAAATTA ACAGCAAAAA TGCAGAGTCT 60
TTTCAGTTTC ACACTGAAGA TTATTTTGGT AAGGAAAGTT TATGGACTGG AAAAGGAATA 120
CAGTGGCTG ATGGTGGATG GCTCATACCC TCCAATGATG GAAAGGCTGG AAAAGAAGAA 180
TTTATATAG 188

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 229...10482
(D) OTHER INFORMATION: BRCA2 (OMI1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CCTGTGGCA CTGCTGCGCC 60
TCTGCTGCGC CTCGGGTGTC TTTTGGGCG GTGGGTGCGC GCCGGGAGAA GCGTGAGGGG 120
ACAGATTTGT GACCGGCGCG GTTTTGTCA GCTTACTCC GCCAAAAAG AACTGCACCT 180
20 CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCCT AGGTAAAA ATG CCT ATT 237
Met Pro Ile
1
GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC 285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
5 10 15
AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT 333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu
20 25 30 35
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA 381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu
40 45 50
35 CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG 429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg
55 60 65
40 AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG 477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu
70 75 80
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT 525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp
85 90 95
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA 573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys
100 105 110 115
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC 621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser
120 125 130
55 TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA 669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln
135 140 145
60 TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT 717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser
150 155 160

66330" T 2448000

Sub
Q1

5	TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	765
	165 170 175	
10	ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	813
	180 185 190 195	
15	AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	861
	200 205 210	
20	AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	909
	215 220 225	
25	AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	957
	230 235 240	
30	GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg	1005
	245 250 255	
35	GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys	1053
	260 265 270 275	
40	GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA AAT GTC CTA Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro Asn Val Leu	1101
	280 285 290	
45	GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser	1149
	295 300 305	
50	TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val	1197
	310 315 320	
55	AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp	1245
	325 330 335	
60	GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val	1293
	340 345 350 355	
65	TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala	1341
	360 365 370	
70	CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val	1389
	375 380 385	
75	GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu	1437
	390 395 400	

5 AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT 1485
 Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys
 405 410 415
 GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA 1533
 Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg
 420 425 430 435
 10 AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC 1581
 Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser
 440 445 450
 15 CTA CCA AAA TCA GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG 1629
 Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys
 455 460 465
 AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA 1677
 Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala
 470 475 480
 20 GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG 1725
 Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln
 485 490 495
 25 GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT 1773
 Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr
 500 505 510 515
 30 TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA 1821
 Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys
 520 525 530
 35 GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA 1869
 Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser
 535 540 545
 40 CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG 1917
 Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp
 550 555 560
 45 CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA 1965
 Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu
 565 570 575
 ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT 2013
 Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His
 580 585 590 595
 50 GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA 2061
 Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser
 600 605 610
 55 GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA 2109
 Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala
 615 620 625
 60 CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG 2157
 Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val
 630 635 640
 AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA 2205

Sub
A1

	Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr	Leu	Ser	Leu	
	645						650					655					
5	ACT	AGC	TCT	TTT	GGG	ACA	ATT	CTG	AGG	AAA	TGT	TCT	AGA	AAT	GAA	ACA	2253
	Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg	Asn	Glu	Thr	
	660					665					670				675		
10	TGT	TCT	AAT	AAT	ACA	GTA	ATC	TCT	CAG	GAT	CTT	GAT	TAT	AAA	GAA	GCA	2301
	Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr	Lys	Glu	Ala	
					680					685					690		
15	AAA	TGT	AAT	AAG	GAA	AAA	CTA	CAG	TTA	TTT	ATT	ACC	CCA	GAA	GCT	GAT	2349
	Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro	Glu	Ala	Asp	
				695				700						705			
20	TCT	CTG	TCA	TGC	CTG	CAG	GAA	GGA	CAG	TGT	GAA	AAT	GAT	CCA	AAA	AGC	2397
	Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp	Pro	Lys	Ser	
			710					715					720				
25	AAA	AAA	GTT	TCA	GAT	ATA	AAA	GAA	GAG	GTC	TTG	GCT	GCA	GCA	TGT	CAC	2445
	Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala	Ala	Cys	His	
			725				730					735					
30	CCA	GTA	CAA	CAT	TCA	AAA	GTG	GAA	TAC	AGT	GAT	ACT	GAC	TTT	CAA	TCC	2493
	Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp	Phe	Gln	Ser	
	740					745					750				755		
35	CAG	AAA	AGT	CTT	TTA	TAT	GAT	CAT	GAA	AAT	GCC	AGC	ACT	CTT	ATT	TTA	2541
	Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr	Leu	Ile	Leu	
					760					765					770		
40	ACT	CCT	ACT	TCC	AAG	GAT	GTT	CTG	TCA	AAC	CTA	GTC	ATG	ATT	TCT	AGA	2589
	Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met	Ile	Ser	Arg	
				775				780						785			
45	GGC	AAA	GAA	TCA	TAC	AAA	ATG	TCA	GAC	AAG	CTC	AAA	GGT	AAC	AAT	TAT	2637
	Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly	Asn	Asn	Tyr	
			790				795						800				
50	GAA	TCT	GAT	GTT	GAA	TTA	ACC	AAA	AAT	ATT	CCC	ATG	GAA	AAG	AAT	CAA	2685
	Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu	Lys	Asn	Gln	
			805				810					815					
55	GAT	GTA	TGT	GCT	TTA	AAT	GAA	AAT	TAT	AAA	AAC	GTT	GAG	CTG	TTG	CCA	2733
	Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu	Leu	Leu	Pro	
	820					825					830				835		
60	CCT	GAA	AAA	TAC	ATG	AGA	GTA	GCA	TCA	CCT	TCA	AGA	AAG	GTA	CAA	TTC	2781
	Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys	Val	Gln	Phe	
					840					845					850		
65	AAC	CAA	AAC	ACA	AAT	CTA	AGA	GTA	ATC	CAA	AAA	AAT	CAA	GAA	GAA	ACT	2829
	Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln	Glu	Glu	Thr	
				855					860					865			
70	ACT	TCA	ATT	TCA	AAA	ATA	ACT	GTC	AAT	CCA	GAC	TCT	GAA	GAA	CTT	TTC	2877
	Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu	Glu	Leu	Phe	
				870				875					880				
75	TCA	GAC	AAT	GAG	AAT	AAT	TTT	GTC	TTC	CAA	GTA	GCT	AAT	GAA	AGG	AAT	2925
	Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Val	Ala	Asn	Glu	Arg	Asn	

00044-05230

Sub
a1

	885	890	895	
5	AAT CTT GCT TTA GGA Asn Leu Ala Leu Gly 900	AAT ACT AAG GAA CTT Asn Thr Lys Glu Leu 905	CAT GAA ACA GAC TTG ACT Glu Thr Asp Leu Thr 910	2973
10	TGT GTA AAC GAA CCC Cys Val Asn Glu Pro 920	ATT TTC AAG AAC TCT Ile Phe Lys Asn Ser 925	ACC ATG GTT TTA TAT GGA Thr Met Val Leu Tyr Gly 930	3021
15	GAC ACA GGT GAT AAA Asp Thr Gly Asp Lys 935	CAA GCA ACC CAA GTG Gln Ala Thr Gln Val 940	TCA ATT AAA AAA GAT TTG Ile Lys Lys Asp Leu 945	3069
20	GTT TAT GTT CTT GCA Val Tyr Val Leu Ala 950	GAG GAG AAC AAA AAT Glu Glu Asn Lys Asn 955	AGT GTA AAG CAG CAT ATA Ser Val Lys Gln His Ile 960	3117
25	AAA ATG ACT CTA GGT Lys Met Thr Leu Gly 965	CAA GAT TTA AAA TCG Gln Asp Leu Lys Ser 970	GAC ATC TCC TTG AAT ATA Asp Ile Ser Leu Asn Ile 975	3165
30	GAT AAA ATA CCA GAA Asp Lys Ile Pro Glu 980	AAA AAT AAT GAT TAC Lys Asn Asn Asp Tyr 985	ATG AAC AAA TGG GCA GGA Met Asn Lys Trp Ala Gly 990	3213
35	CTC TTA GGT CCA ATT Leu Leu Gly Pro Ile 1000	TCA AAT CAC AGT TTT Ser Asn His Ser Phe 1005	GGA GGT AGC TTC AGA ACA Gly Gly Ser Phe Arg Thr 1010	3261
40	GCT TCA AAT AAG GAA Ala Ser Asn Lys Glu 1015	ATC AAG CTC TCT GAA Ile Lys Leu Ser Glu 1020	CAT AAC ATT AAG AAG AGC His Asn Ile Lys Lys Ser 1025	3309
45	AAA ATG TTC TTC AAA Lys Met Phe Phe Lys 1030	GAT ATT GAA GAA CAA Asp Ile Glu Glu Gln 1035	TAT CCT ACT AGT TTA GCT Tyr Pro Thr Ser Leu Ala 1040	3357
50	TGT GTT GAA ATT GTA Cys Val Glu Ile Val 1045	AAT ACC TTG GCA TTA Asn Thr Leu Ala Leu 1050	GAT AAT CAA AAG AAA CTG Asp Asn Gln Lys Lys Leu 1055	3405
55	AGC AAG CCT CAG TCA Ser Lys Pro Gln Ser 1060	ATT AAT ACT GTA TCT Ile Asn Thr Val Ser 1065	CAT TTA CAG AGT AGT Ala His Leu Gln Ser Ser 1070	3453
60	GTA GTT GTT TCT GAT Val Val Val Ser Asp 1080	TGT AAA AAT AGT CAT Cys Lys Asn Ser His 1085	ATA ACC CCT CAG ATG TTA Ile Thr Pro Gln Met Leu 1090	3501
65	TTT TCC AAG CAG GAT Phe Ser Lys Gln Asp 1095	TTT AAT TCA AAC CAT Phe Asn Ser Asn His 1100	AAT TTA ACA CCT AGC CAA Leu Thr Pro Ser Gln 1105	3549
70	AAG GCA GAA ATT ACA Lys Ala Glu Ile Thr 1110	GAA CTT TCT ACT ATA Glu Leu Ser Thr Ile 1115	TTA GAA GAA TCA GGA AGT Leu Glu Glu Ser Gly Ser 1120	3597
75	CAG TTT GAA TTT ACT Gln Phe Glu Phe Thr 1125	CAG TTT AGA AAA CCA Gln Phe Arg Lys Pro 1130	AGC TAC ATA TTG CAG AAG Ser Tyr Ile Leu Gln Lys 1135	3645

Sub
a

	AGT	ACA	TTT	GAA	GTG	CCT	GAA	AAC	CAG	ATG	ACT	ATC	TTA	AAG	ACC	ACT	
	Ser	Thr	Phe	Glu	Val	Pro	Glu	Asn	Gln	Met	Thr	Ile	Leu	Lys	Thr	Thr	
5	1140					1145					1150					1155	3693
	TCT	GAG	GAA	TGC	AGA	GAT	GCT	GAT	CTT	CAT	GTC	ATA	ATG	AAT	GCC	CCA	3741
	Ser	Glu	Glu	Cys	Arg	Asp	Ala	Asp	Leu	His	Val	Ile	Met	Asn	Ala	Pro	
				1160					1165						1170		
10	TCG	ATT	GGT	CAG	GTA	GAC	AGC	AGC	AAG	CAA	TTT	GAA	GGT	ACA	GTT	GAA	3789
	Ser	Ile	Gly	Gln	Val	Asp	Ser	Ser	Lys	Gln	Phe	Glu	Gly	Thr	Val	Glu	
				1175					1180					1185			
15	ATT	AAA	CGG	AAG	TTT	GCT	GGC	CTG	TTG	AAA	AAT	GAC	TGT	AAC	AAA	AGT	3837
	Ile	Lys	Arg	Lys	Phe	Ala	Gly	Leu	Leu	Lys	Asn	Asp	Cys	Asn	Lys	Ser	
			1190					1195					1200				
20	GCT	TCT	GGT	TAT	TTA	ACA	GAT	GAA	AAT	GAA	GTG	GGG	TTT	AGG	GGC	TTT	3885
	Ala	Ser	Gly	Tyr	Leu	Thr	Asp	Glu	Asn	Glu	Val	Gly	Phe	Arg	Gly	Phe	
			1205				1210					1215					
	TAT	TCT	GCT	CAT	GGC	ACA	AAA	CTG	AAT	GTT	TCT	ACT	GAA	GCT	CTG	CAA	3933
	Tyr	Ser	Ala	His	Gly	Thr	Lys	Leu	Asn	Val	Ser	Thr	Glu	Ala	Leu	Gln	
25	1220					1225					1230					1235	
	AAA	GCT	GTG	AAA	CTG	TTT	AGT	GAT	ATT	GAG	AAT	ATT	AGT	GAG	GAA	ACT	3981
	Lys	Ala	Val	Lys	Leu	Phe	Ser	Asp	Ile	Glu	Asn	Ile	Ser	Glu	Glu	Thr	
				1240						1245					1250		
30	TCT	GCA	GAG	GTA	CAT	CCA	ATA	AGT	TTA	TCT	TCA	AGT	AAA	TGT	CAT	GAT	4029
	Ser	Ala	Glu	Val	His	Pro	Ile	Ser	Leu	Ser	Ser	Ser	Lys	Cys	His	Asp	
				1255					1260					1265			
35	TCT	GTT	GTT	TCA	ATG	TTT	AAG	ATA	GAA	AAT	CAT	AAT	GAT	AAA	ACT	GTA	4077
	Ser	Val	Val	Ser	Met	Phe	Lys	Ile	Glu	Asn	His	Asn	Asp	Lys	Thr	Val	
			1270				1275						1280				
40	AGT	GAA	AAA	AAT	AAT	AAA	TGC	CAA	CTG	ATA	TTA	CAA	AAT	AAT	ATT	GAA	4125
	Ser	Glu	Lys	Asn	Asn	Lys	Cys	Gln	Leu	Ile	Leu	Gln	Asn	Asn	Ile	Glu	
		1285					1290					1295					
45	ATG	ACT	ACT	GGC	ACT	TTT	GTT	GAA	GAA	ATT	ACT	GAA	AAT	TAC	AAG	AGA	4173
	Met	Thr	Thr	Gly	Thr	Phe	Val	Glu	Glu	Ile	Thr	Glu	Asn	Tyr	Lys	Arg	
	1300					1305					1310					1315	
	AAT	ACT	GAA	AAT	GAA	GAT	AAC	AAA	TAT	ACT	GCT	GCC	AGT	AGA	AAT	TCT	4221
	Asn	Thr	Glu	Asn	Glu	Asp	Asn	Lys	Tyr	Thr	Ala	Ala	Ser	Arg	Asn	Ser	
				1320					1325					1330			
50	CAT	AAC	TTA	GAA	TTT	GAT	GGC	AGT	GAT	TCA	AGT	AAA	AAT	GAT	ACT	GTT	4269

0604450744000

Sub
a1

	Leu	Cys	Arg	Gln	Thr	Glu	Asn	Leu	Lys	Thr	Ser	Lys	Ser	Ile	Phe	Leu	
	1620					1625					1630					1635	
5	AAA	GTT	AAA	GTA	CAT	GAA	AAT	GTA	GAA	AAA	GAA	ACA	GCA	AAA	AGT	CCT	5181
	Lys	Val	Lys	Val	His	Glu	Asn	Val	Glu	Lys	Glu	Thr	Ala	Lys	Ser	Pro	
					1640					1645					1650		
10	GCA	ACT	TGT	TAC	ACA	AAT	CAG	TCC	CCT	TAT	TCA	GTC	ATT	GAA	AAT	TCA	5229
	Ala	Thr	Cys	Tyr	Thr	Asn	Gln	Ser	Pro	Tyr	Ser	Val	Ile	Glu	Asn	Ser	
					1655				1660					1665			
15	GCC	TTA	GCT	TTT	TAC	ACA	AGT	TGT	AGT	AGA	AAA	ACT	TCT	GTG	AGT	CAG	5277
	Ala	Leu	Ala	Phe	Tyr	Thr	Ser	Cys	Ser	Arg	Lys	Thr	Ser	Val	Ser	Gln	
					1670				1675					1680			
20	ACT	TCA	TTA	CTT	GAA	GCA	AAA	AAA	TGG	CTT	AGA	GAA	GGA	ATA	TTT	GAT	5325
	Thr	Ser	Leu	Leu	Glu	Ala	Lys	Lys	Trp	Leu	Arg	Glu	Gly	Ile	Phe	Asp	
		1685					1690					1695					
25	GGT	CAA	CCA	GAA	AGA	ATA	AAT	ACT	GCA	GAT	TAT	GTA	GGA	AAT	TAT	TTG	5373
	Gly	Gln	Pro	Glu	Arg	Ile	Asn	Thr	Ala	Asp	Tyr	Val	Gly	Asn	Tyr	Leu	
	1700					1705					1710					1715	
30	TAT	GAA	AAT	AAT	TCA	AAC	AGT	ACT	ATA	GCT	GAA	AAT	GAC	AAA	AAT	CAT	5421
	Tyr	Glu	Asn	Asn	Ser	Asn	Ser	Thr	Ile	Ala	Glu	Asn	Asp	Lys	Asn	His	
					1720					1725					1730		
35	CTC	TCC	GAA	AAA	CAA	GAT	ACT	TAT	TTA	AGT	AAC	AGT	AGC	ATG	TCT	AAC	5469
	Leu	Ser	Glu	Lys	Gln	Asp	Thr	Tyr	Leu	Ser	Asn	Ser	Ser	Met	Ser	Asn	
					1735				1740					1745			
40	AGC	TAT	TCC	TAC	CAT	TCT	GAT	GAG	GTA	TAT	AAT	GAT	TCA	GGA	TAT	CTC	5517
	Ser	Tyr	Ser	Tyr	His	Ser	Asp	Glu	Val	Tyr	Asn	Asp	Ser	Gly	Tyr	Leu	
			1750				1755						1760				
45	TCA	AAA	AAT	AAA	CTT	GAT	TCT	GGT	ATT	GAG	CCA	GTA	TTG	AAG	AAT	GTT	5565
	Ser	Lys	Asn	Lys	Leu	Asp	Ser	Gly	Ile	Glu	Pro	Val	Leu	Lys	Asn	Val	
		1765					1770					1775					
50	GAA	GAT	CAA	AAA	AAC	ACT	AGT	TTT	TCC	AAA	GTA	ATA	TCC	AAT	GTA	AAA	5613
	Glu	Asp	Gln	Lys	Asn	Thr	Ser	Phe	Ser	Lys	Val	Ile	Ser	Asn	Val	Lys	
	1780					1785					1790				1795		
55	GAT	GCA	AAT	GCA	TAC	CCA	CAA	ACT	GTA	AAT	GAA	GAT	ATT	TGC	GTT	GAG	5661
	Asp	Ala	Asn	Ala	Tyr	Pro	Gln	Thr	Val	Asn	Glu	Asp	Ile	Cys	Val	Glu	
					1800					1805					1810		
60	GAA	CTT	GTG	ACT	AGC	TCT	TCA	CCC	TGC	AAA	AAT	AAA	AAT	GCA	GCC	ATT	5709
	Glu	Leu	Val	Thr	Ser	Ser	Ser	Pro	Cys	Lys	Asn	Lys	Asn	Ala	Ala	Ile	
				1815					1820					1825			
65	AAA	TTG	TCC	ATA	TCT	AAT	AGT	AAT	AAT	TTT	GAG	GTA	GGG	CCA	CCT	GCA	5757
	Lys	Leu	Ser	Ile	Ser	Asn	Ser	Asn	Asn	Phe	Glu	Val	Gly	Pro	Pro	Ala	
			1830					1835					1840				
70	TTT	AGG	ATA	GCC	AGT	GGT	AAA	ATC	GTT	TGT	GTT	TCA	CAT	GAA	ACA	ATT	5805
	Phe	Arg	Ile	Ala	Ser	Gly	Lys	Ile	Val	Cys	Val	Ser	His	Glu	Thr	Ile	
		1845					1850					1855					
75	AAA	AAA	GTG	AAA	GAC	ATA	TTT	ACA	GAC	AGT	TTC	AGT	AAA	GTA	ATT	AAG	5853
	Lys	Lys	Val	Lys	Asp	Ile	Phe	Thr	Asp	Ser	Phe	Ser	Lys	Val	Ile	Lys	

	1860	1865	1870	1875	
5	GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala	1880	1885	1890	5901
10	GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser	1895	1900	1905	5949
15	CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp	1910	1915	1920	5997
20	ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu	1925	1930	1935	6045
25	GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser	1940	1945	1950	6093
30	GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser	1960	1965	1970	6141
35	GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln	1975	1980	1985	6189
40	GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile	1990	1995	2000	6237
45	GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn	2005	2010	2015	6285
50	GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr	2020	2025	2030	6333
55	CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn	2040	2045	2050	6381
60	TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser	2055	2060	2065	6429
	ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe	2070	2075	2080	6477
	GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg	2085	2090	2095	6525
	CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu	2100	2105	2110	6573

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	TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT	7341
	Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser	
	2360 2365 2370	
5	TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT	7389
	Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala	
	2375 2380 2385	
10	ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC	7437
	Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr	
	2390 2395 2400	
15	AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT	7485
	Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val	
	2405 2410 2415	
20	GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA	7533
	Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln	
	2420 2425 2430 2435	
	AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC	7581
	Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp	
	2440 2445 2450	
25	AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT	7629
	Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala	
	2455 2460 2465	
30	GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT	7677
	Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser	
	2470 2475 2480	
35	CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA	7725
	Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln	
	2485 2490 2495	
40	AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA	7773
	Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr	
	2500 2505 2510 2515	
45	TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT	7821
	Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val	
	2520 2525 2530	
	CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA	7869
	Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys	
	2535 2540 2545	
50	CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC	7917
	His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His	
	2550 2555 2560	
55	ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA	7965
	Thr Gln Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile	
	2565 2570 2575	
60	CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT	8013
	Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala	
	2580 2585 2590 2595	
	GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT	8061

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	Gly	Lys	Glu	Glu	Phe	Tyr	Arg	Ala	Leu	Cys	Asp	Thr	Pro	Gly	Val	Asp	
					2600					2605						2610	
5	CCA	AAG	CTT	ATT	TCT	AGA	ATT	TGG	GTT	TAT	AAT	CAC	TAT	AGA	TGG	ATC	8109
	Pro	Lys	Leu	Ile	Ser	Arg	Ile	Trp	Val	Tyr	Asn	His	Tyr	Arg	Trp	Ile	
					2615					2620						2625	
10	ATA	TGG	AAA	CTG	GCA	GCT	ATG	GAA	TGT	GCC	TTT	CCT	AAG	GAA	TTT	GCT	8157
	Ile	Trp	Lys	Leu	Ala	Ala	Met	Glu	Cys	Ala	Phe	Pro	Lys	Glu	Phe	Ala	
					2630					2635						2640	
15	AAT	AGA	TGC	CTA	AGC	CCA	GAA	AGG	GTG	CTT	CTT	CAA	CTA	AAA	TAC	AGA	8205
	Asn	Arg	Cys	Leu	Ser	Pro	Glu	Arg	Val	Leu	Leu	Gln	Leu	Lys	Tyr	Arg	
					2645					2650						2655	
20	TAT	GAT	ACG	GAA	ATT	GAT	AGA	AGC	AGA	AGA	TCG	GCT	ATA	AAA	AAG	ATA	8253
	Tyr	Asp	Thr	Glu	Ile	Asp	Arg	Ser	Arg	Arg	Ser	Ala	Ile	Lys	Lys	Ile	
					2660					2665						2675	
25	ATG	GAA	AGG	GAT	GAC	ACA	GCT	GCA	AAA	ACA	CTT	GTT	CTC	TGT	GTT	TCT	8301
	Met	Glu	Arg	Asp	Asp	Thr	Ala	Ala	Lys	Thr	Leu	Val	Leu	Cys	Val	Ser	
					2680					2685						2690	
30	GAC	ATA	ATT	TCA	TTG	AGC	GCA	AAT	ATA	TCT	GAA	ACT	TCT	AGC	AAT	AAA	8349
	Asp	Ile	Ile	Ser	Leu	Ser	Ala	Asn	Ile	Ser	Glu	Thr	Ser	Ser	Asn	Lys	
					2695					2700						2705	
35	ACT	AGT	AGT	GCA	GAT	ACC	CAA	AAA	GTG	GCC	ATT	ATT	GAA	CTT	ACA	GAT	8397
	Thr	Ser	Ser	Ala	Asp	Thr	Gln	Lys	Val	Ala	Ile	Ile	Glu	Leu	Thr	Asp	
					2710					2715						2720	
40	GGG	TGG	TAT	GCT	GTT	AAG	GCC	CAG	TTA	GAT	CCT	CCC	CTC	TTA	GCT	GTC	8445
	Gly	Trp	Tyr	Ala	Val	Lys	Ala	Gln	Leu	Asp	Pro	Pro	Leu	Leu	Ala	Val	
					2725					2730						2735	
45	TTA	AAG	AAT	GGC	AGA	CTG	ACA	GTT	GGT	CAG	AAG	ATT	ATT	CTT	CAT	GGA	8493
	Leu	Lys	Asn	Gly	Arg	Leu	Thr	Val	Gly	Gln	Lys	Ile	Ile	Leu	His	Gly	
					2740					2745						2755	
50	GCA	GAA	CTG	GTG	GGC	TCT	CCT	GAT	GCC	TGT	ACA	CCT	CTT	GAA	GCC	CCA	8541
	Ala	Glu	Leu	Val	Gly	Ser	Pro	Asp	Ala	Cys	Thr	Pro	Leu	Glu	Ala	Pro	
					2760					2765						2770	
55	GAA	TCT	CTT	ATG	TTA	AAG	ATT	TCT	GCT	AAC	AGT	ACT	CGG	CCT	GCT	CGC	8589
	Glu	Ser	Leu	Met	Leu	Lys	Ile	Ser	Ala	Asn	Ser	Thr	Arg	Pro	Ala	Arg	
					2775					2780						2785	
60	TGG	TAT	ACC	AAA	CTT	GGA	TTC	TTT	CCT	GAC	CCT	AGA	CCT	TTT	CCT	CTG	8637
	Trp	Tyr	Thr	Lys	Leu	Gly	Phe	Phe	Pro	Asp	Pro	Arg	Pro	Phe	Pro	Leu	
					2790					2795						2800	
65	CCC	TTA	TCA	TCG	CTT	TTC	AGT	GAT	GGA	GGA	AAT	GTT	GGT	TGT	GTT	GAT	8685
	Pro	Leu	Ser	Ser	Leu	Phe	Ser	Asp	Gly	Gly	Asn	Val	Gly	Cys	Val	Asp	
					2805					2810						2815	
70	GTA	ATT	ATT	CAA	AGA	GCA	TAC	CCT	ATA	CAG	TGG	ATG	GAG	AAG	ACA	TCA	8733
	Val	Ile	Ile	Gln	Arg	Ala	Tyr	Pro	Ile	Gln	Trp	Met	Glu	Lys	Thr	Ser	
					2820					2825						2835	
75	TCT	GGA	TTA	TAC	ATA	TTT	CGC	AAT	GAA	AGA	GAG	GAA	GAA	AAG	GAA	GCA	8781
	Ser	Gly	Leu	Tyr	Ile	Phe	Arg	Asn	Glu	Arg	Glu	Glu	Glu	Lys	Glu	Ala	

2840

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5 GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT 8829
Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr
2855 2860 2865

AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA 8877
Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro
2870 2875 2880

10 TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA 8925
Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln
2885 2890 2895

15 GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT 8973
Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala
2900 2905 2910 2915

20 TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT 9021
Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn
2920 2925 2930

25 CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA 9069
His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu
2935 2940 2945

30 ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA 9117
Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser
2950 2955 2960

AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA 9165
Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys
2965 2970 2975

35 AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT 9213
Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp
2980 2985 2990 2995

40 TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT 9261
Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu
3000 3005 3010

45 GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA 9309
Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu
3015 3020 3025

GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA 9357
Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu
3030 3035 3040

50 ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA 9405
Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys
3045 3050 3055

55 TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA 9453
Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile
3060 3065 3070 3075

60 GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC 9501
Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val
3080 3085 3090

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5	TAT	TTG	TCA	GAC	GAA	TGT	TAC	AAT	TTA	CTG	GCA	ATA	AAG	TTT	TGG	ATA	9549
	Tyr	Leu	Ser	Asp	Glu	Cys	Tyr	Asn	Leu	Leu	Ala	Ile	Lys	Phe	Trp	Ile	
				3095					3100					3105			
10	GAC	CTT	AAT	GAG	GAC	ATT	ATT	AAG	CCT	CAT	ATG	TTA	ATT	GCT	GCA	AGC	9597
	Asp	Leu	Asn	Glu	Asp	Ile	Ile	Lys	Pro	His	Met	Leu	Ile	Ala	Ala	Ser	
				3110				3115					3120				
15	AAC	CTC	CAG	TGG	CGA	CCA	GAA	TCC	AAA	TCA	GGC	CTT	CTT	ACT	TTA	TTT	9645
	Asn	Leu	Gln	Trp	Arg	Pro	Glu	Ser	Lys	Ser	Gly	Leu	Leu	Thr	Leu	Phe	
				3125				3130					3135				
20	GCT	GGA	GAT	TTT	TCT	GTG	TTT	TCT	GCT	AGT	CCA	AAA	GAG	GGC	CAC	TTT	9693
	Ala	Gly	Asp	Phe	Ser	Val	Phe	Ser	Ala	Ser	Pro	Lys	Glu	Gly	His	Phe	
	3140					3145					3150					3155	
25	CAA	GAG	ACA	TTC	AAC	AAA	ATG	AAA	AAT	ACT	GTT	GAG	AAT	ATT	GAC	ATA	9741
	Gln	Glu	Thr	Phe	Asn	Lys	Met	Lys	Asn	Thr	Val	Glu	Asn	Ile	Asp	Ile	
					3160					3165					3170		
30	CTT	TGC	AAT	GAA	GCA	GAA	AAC	AAG	CTT	ATG	CAT	ATA	CTG	CAT	GCA	AAT	9789
	Leu	Cys	Asn	Glu	Ala	Glu	Asn	Lys	Leu	Met	His	Ile	Leu	His	Ala	Asn	
				3175					3180					3185			
35	GAT	CCC	AAG	TGG	TCC	ACC	CCA	ACT	AAA	GAC	TGT	ACT	TCA	GGG	CCG	TAC	9837
	Asp	Pro	Lys	Trp	Ser	Thr	Pro	Thr	Lys	Asp	Cys	Thr	Ser	Gly	Pro	Tyr	
				3190					3195					3200			
40	ACT	GCT	CAA	ATC	ATT	CCT	GGT	ACA	GGA	AAC	AAG	CTT	CTG	ATG	TCT	TCT	9885
	Thr	Ala	Gln	Ile	Ile	Pro	Gly	Thr	Gly	Asn	Lys	Leu	Leu	Met	Ser	Ser	
				3205				3210					3215				
45	CCT	AAT	TGT	GAG	ATA	TAT	TAT	CAA	AGT	CCT	TTA	TCA	CTT	TGT	ATG	GCC	9933
	Pro	Asn	Cys	Glu	Ile	Tyr	Tyr	Gln	Ser	Pro	Leu	Ser	Leu	Cys	Met	Ala	
	3220					3225					3230					3235	
50	AAA	AGG	AAG	TCT	GTT	TCC	ACA	CCT	GTC	TCA	GCC	CAG	ATG	ACT	TCA	AAG	9981
	Lys	Arg	Lys	Ser	Val	Ser	Thr	Pro	Val	Ser	Ala	Gln	Met	Thr	Ser	Lys	
					3240					3245					3250		
55	TCT	TGT	AAA	GGG	GAG	AAA	GAG	ATT	GAT	GAC	CAA	AAG	AAC	TGC	AAA	AAG	10029
	Ser	Cys	Lys	Gly	Glu	Lys	Glu	Ile	Asp	Asp	Gln	Lys	Asn	Cys	Lys	Lys	
				3255					3260					3265			
60	AGA	AGA	GCC	TTG	GAT	TTC	TTG	AGT	AGA	CTG	CCT	TTA	CCT	CCA	CCT	GTT	10077
	Arg	Arg	Ala	Leu	Asp	Phe	Leu	Ser	Arg	Leu	Pro	Leu	Pro	Pro	Pro	Val	
				3270				3275					3280				
65	AGT	CCC	ATT	TGT	ACA	TTT	GTT	TCT	CCG	GCT	GCA	CAG	AAG	GCA	TTT	CAG	10125

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06250.2448060

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TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA 10269
Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile
3335 3340 3345

5

AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA 10317
Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile
3350 3355 3360

10

TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT 10365
Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr
3365 3370 3375

15

CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413
Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu
3380 3385 3390 3395

20

AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461
Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr
3400 3405 3410

25

ATT ACA ACT AAA AAA TAT ATC TAA 10485
Ile Thr Thr Lys Lys Tyr Ile
3415

(2) INFORMATION FOR SEQ ID NO:5:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3418 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

- (ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys
1 5 10 15

Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe
20 25 30

45

Glu Glu Leu Ser Ser Glu Ala Pro Tyr Asn Ser Glu Pro Ala Glu
35 40 45

Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
50 55 60

Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
65 70 75 80

50

Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
85 90 95

Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
100 105 110

55

Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
115 120 125

Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
130 135 140

Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
145 150 155 160

60

Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
165 170 175

Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met

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Sub
A1

					180				185				190
	Ser	Trp	Ser	Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser
			195					200				205	
5	Leu	Ile	Val	Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe
		210					215					220	
	Thr	Thr	Ala	Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp
	225					230				235			240
10	Lys	Lys	Asn	Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser
					245					250			255
	Asn	Gln	Arg	Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr
				260					265				270
	Ser	Phe	Lys	Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys
			275					280				285	
15	Asn	Val	Leu	Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp
		290					295				300		
	Glu	Asp	Ser	Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr
	305					310					315		
	Gln	Lys	Val	Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe
					325					330			335
20	Asn	Ala	Asp	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys
					340				345				350
	Ser	Phe	Val	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro
			355					360				365	
25	Asn	Val	Ala	His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp
		370					375					380	
	Lys	Glu	Val	Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln
		385				390				395			400
	Ser	Gly	Leu	Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu
				405					410				415
30	Ser	Ser	Cys	Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu
				420					425				430
	Asn	Lys	Arg	Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser
			435					440				445	
35	Ile	Ser	Ser	Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu
		450					455				460		
	Val	Asn	Lys	Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His
		465				470				475			480
	Ile	Leu	Ala	Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro
				485					490				495
40	Ser	Phe	Gln	Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg
			500						505				510
	Lys	Glu	Thr	Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr
			515					520				525	
45	Phe	Lys	Lys	Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu
		530					535				540		
	Val	Cys	Ser	Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu
		545				550				555			560
	Gly	Ser	Trp	Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala
				565					570				575
50	Ala	Gly	Leu	Ile	Ser	Thr	Leu	Lys	Lys	Lys	Thr	Asn	Lys
			580						585				590
	Ala	Ile	His	Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile
			595					600				605	
55	Gln	Lys	Ser	Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu
		610					615				620		
	Phe	Glu	Ala	Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly
		625				630				635			640
	Ser	Ser	Val	Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu
				645						650			655
60	Leu	Ser	Leu	Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys
				660					665				670

5 Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
 675 680 685
 Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
 690 695 700
 Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
 705 710 715 720
 Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
 725 730 735
 10 Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
 740 745 750
 Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
 755 760 765
 15 Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
 770 775 780
 Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
 785 790 795 800
 Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
 805 810 815
 20 Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
 820 825 830
 Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
 835 840 845
 25 Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
 850 855 860
 Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
 865 870 875 880
 Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
 885 890 895
 30 Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
 900 905 910
 Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
 915 920 925
 35 Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
 930 935 940
 Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
 945 950 955 960
 Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
 965 970 975
 40 Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys
 980 985 990
 Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
 995 1000 1005
 45 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
 1010 1015 1020
 Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
 1025 1030 1035 104
 Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
 1045 1050 1055
 50 Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
 1060 1065 1070
 Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
 1075 1080 1085
 55 Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
 1090 1095 1100
 Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
 1105 1110 1115 112
 Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
 1125 1130 1135
 60 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
 1140 1145 1150
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Ile Met

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Sub
Al

	1155		1160		1165
	Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly				
	1170		1175		1180
5	Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys				
	1185		1190		1195
	Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe				120
		1205		1210	
	Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu				1215
10		1220		1225	
	Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser				1230
		1235		1240	
	Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys				1245
		1250		1255	
	Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp				1260
15		1265		1270	
	Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn				1275
		1285		1290	
	Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn				1295
20		1300		1305	
	Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser				1310
		1315		1320	
	Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn				1325
		1330		1335	
	Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp				1340
25		1345		1350	
	Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly				1355
		1365		1370	
	Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val				1375
30		1380		1385	
	Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln				1390
		1395		1400	
	Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser				1405
		1410		1415	
	Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys				1420
35		1425		1430	
	Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu				1435
		1445		1450	
	Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys				1455
40		1460		1465	
	Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His				1470
		1475		1480	
	Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val				1485
		1490		1495	
	Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr				1500
45		1505		1510	
	Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys				1515
		1525		1530	
	Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly				1535
50		1540		1545	
	Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys				1550
		1555		1560	
	Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu				1565
		1570		1575	
	Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn				1580
55		1585		1590	
	Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu				1595
		1605		1610	
	Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser				1615
60		1620		1625	
	Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala				1630
		1635		1640	
					1645

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Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
 1650 1655 1660
 Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
 1665 1670 1675 168
 Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
 1685 1690 1695
 Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
 1700 1705 1710
 Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
 1715 1720 1725
 Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
 1730 1735 1740
 Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
 1745 1750 1755 176
 Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
 1765 1770 1775
 Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
 1780 1785 1790
 Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
 1795 1800 1805
 Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn
 1810 1815 1820
 Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly
 1825 1830 1835 184
 Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
 1845 1850 1855
 Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
 1860 1865 1870
 Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
 1875 1880 1885
 Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
 1890 1895 1900
 His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
 1905 1910 1915 192
 Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
 1925 1930 1935
 Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
 1940 1945 1950
 Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
 1955 1960 1965
 Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
 1970 1975 1980
 Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe
 1985 1990 1995 200
 Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
 2005 2010 2015
 Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
 2020 2025 2030
 Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
 2035 2040 2045
 Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
 2050 2055 2060
 Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
 2065 2070 2075 208
 Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
 2085 2090 2095
 Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
 2100 2105 2110
 Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
 2115 2120 2125
 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu

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862250 T 448060

2130 2135 2140
 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
 2145 2150 2155 216
 5 Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
 2165 2170 2175
 Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
 2180 2185 2190
 10 Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
 2195 2200 2205
 Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
 2210 2215 2220
 Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
 2225 2230 2235 224
 15 Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
 2245 2250 2255
 Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
 2260 2265 2270
 20 Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
 2275 2280 2285
 Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
 2290 2295 2300
 Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
 2305 2310 2315 232
 25 Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
 2325 2330 2335
 Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
 2340 2345 2350
 30 Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
 2355 2360 2365
 Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
 2370 2375 2380
 Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly
 2385 2390 2395 240
 35 Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
 2405 2410 2415
 His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg
 2420 2425 2430
 Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys
 2435 2440 2445
 40 Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln
 2450 2455 2460
 Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu
 2465 2470 2475 248
 45 Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys
 2485 2490 2495
 Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu
 2500 2505 2510
 Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly
 2515 2520 2525
 50 Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly
 2530 2535 2540
 Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe
 2545 2550 2555 256
 55 Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly
 2565 2570 2575
 Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp
 2580 2585 2590
 Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro
 2595 2600 2605
 60 Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr
 2610 2615 2620

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Sub
a

	Arg	Trp	Ile	Ile	Trp	Lys	Leu	Ala	Ala	Met	Glu	Cys	Ala	Phe	Pro	Lys
	2625					2630					2635					264
5	Glu	Phe	Ala	Asn	Arg	Cys	Leu	Ser	Pro	Glu	Arg	Val	Leu	Leu	Gln	Leu
					2645					2650					2655	
	Lys	Tyr	Arg	Tyr	Asp	Thr	Glu	Ile	Asp	Arg	Ser	Arg	Arg	Ser	Ala	Ile
					2660					2665					2670	
	Lys	Lys	Ile	Met	Glu	Arg	Asp	Asp	Thr	Ala	Ala	Lys	Thr	Leu	Val	Leu
					2675					2680					2685	
10	Cys	Val	Ser	Asp	Ile	Ile	Ser	Leu	Ser	Ala	Asn	Ile	Ser	Glu	Thr	Ser
		2690						2695						2700		
	Ser	Asn	Lys	Thr	Ser	Ser	Ala	Asp	Thr	Gln	Lys	Val	Ala	Ile	Ile	Glu
	2705							2710						2715		272
	Leu	Thr	Asp	Gly	Trp	Tyr	Ala	Val	Lys	Ala	Gln	Leu	Asp	Pro	Pro	Leu
					2725					2730					2735	
15	Leu	Ala	Val	Leu	Lys	Asn	Gly	Arg	Leu	Thr	Val	Gly	Gln	Lys	Ile	Ile
					2740					2745					2750	
	Leu	His	Gly	Ala	Glu	Leu	Val	Gly	Ser	Pro	Asp	Ala	Cys	Thr	Pro	Leu
					2755					2760				2765		
20	Glu	Ala	Pro	Glu	Ser	Leu	Met	Leu	Lys	Ile	Ser	Ala	Asn	Ser	Thr	Arg
					2770					2775					2780	
	Pro	Ala	Arg	Trp	Tyr	Thr	Lys	Leu	Gly	Phe	Phe	Pro	Asp	Pro	Arg	Pro
	2785							2790						2795		280
25	Phe	Pro	Leu	Pro	Leu	Ser	Ser	Leu	Phe	Ser	Asp	Gly	Gly	Asn	Val	Gly
					2805					2810					2815	
	Cys	Val	Asp	Val	Ile	Ile	Gln	Arg	Ala	Tyr	Pro	Ile	Gln	Trp	Met	Glu
					2820					2825					2830	
	Lys	Thr	Ser	Ser	Gly	Leu	Tyr	Ile	Phe	Arg	Asn	Glu	Arg	Glu	Glu	Glu
					2835					2840					2845	
30	Lys	Glu	Ala	Ala	Lys	Tyr	Val	Glu	Ala	Gln	Gln	Lys	Arg	Leu	Glu	Ala
					2850					2855					2860	
	Leu	Phe	Thr	Lys	Ile	Gln	Glu	Glu	Phe	Glu	Glu	His	Glu	Glu	Asn	Thr
	2865							2870							2875	288
	Thr	Lys	Pro	Tyr	Leu	Pro	Ser	Arg	Ala	Leu	Thr	Arg	Gln	Gln	Val	Arg
35					2885					2890					2895	
	Ala	Leu	Gln	Asp	Gly	Ala	Glu	Leu	Tyr	Glu	Ala	Val	Lys	Asn	Ala	Ala
					2900					2905					2910	
	Asp	Pro	Ala	Tyr	Leu	Glu	Gly	Tyr	Phe	Ser	Glu	Glu	Gln	Leu	Arg	Ala
					2915					2920					2925	
40	Leu	Asn	Asn	His	Arg	Gln	Met	Leu	Asn	Asp	Lys	Lys	Gln	Ala	Gln	Ile
					2930					2935					2940	
	Gln	Leu	Glu	Ile	Arg	Lys	Ala	Met	Glu	Ser	Ala	Glu	Gln	Lys	Glu	Gln
	2945							2950							2955	296
	Gly	Leu	Ser	Arg	Asp	Val	Thr	Thr	Val	Trp	Lys	Leu	Arg	Ile	Val	Ser
45					2965					2970					2975	
	Tyr	Ser	Lys	Lys	Glu	Lys	Asp	Ser	Val	Ile	Leu	Ser	Ile	Trp	Arg	Pro
					2980					2985					2990	
	Ser	Ser	Asp	Leu	Tyr	Ser	Leu	Leu	Thr	Glu	Gly	Lys	Arg	Tyr	Arg	Ile
					2995					3000					3005	
50	Tyr	His	Leu	Ala	Thr	Ser	Lys	Ser	Lys	Ser	Lys	Ser	Glu	Arg	Ala	Asn
					3010					3015					3020	
	Ile	Gln	Leu	Ala	Ala	Thr	Lys	Lys	Thr	Gln	Tyr	Gln	Gln	Leu	Pro	Val
	3025							3030							3035	304
	Ser	Asp	Glu	Ile	Leu	Phe	Gln	Ile	Tyr	Gln	Pro	Arg	Glu	Pro	Leu	His
55					3045					3050					3055	
	Phe	Ser	Lys	Phe	Leu	Asp	Pro	Asp	Phe	Gln	Pro	Ser	Cys	Ser	Glu	Val
					3060					3065					3070	
	Asp	Leu	Ile	Gly	Phe	Val	Val	Ser	Val	Val	Lys	Lys	Thr	Gly	Leu	Ala
					3075					3080					3085	
60	Pro	Phe	Val	Tyr	Leu	Ser	Asp	Glu	Cys	Tyr	Asn	Leu	Leu	Ala	Ile	Lys
					3090					3095					3100	
	Phe	Trp	Ile	Asp	Leu	Asn	Glu	Asp	Ile	Ile	Lys	Pro	His	Met	Leu	Ile

Sub
a1

3105 3110 3115 312
Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
3125 3130 3135
5 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
3140 3145 3150
Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
3155 3160 3165
Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
3170 3175 3180
His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
3185 3190 3195 320
Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
3205 3210 3215
15 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
3220 3225 3230
Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
3235 3240 3245
20 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn
3250 3255 3260
Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro
3265 3270 3275 328
Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys
3285 3290 3295
25 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile
3300 3305 3310
Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe
3315 3320 3325
30 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu
3330 3335 3340
Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys
3345 3350 3355 336
Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser
3365 3370 3375
35 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys
3380 3385 3390
Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys
3395 3400 3405
40 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile
3410 3415

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 229...10482
(D) OTHER INFORMATION: BRCA2 (OMI2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC 60
TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGGGTGCGC GCCGGGAGAA GCGTGAGGGG 120
ACAGATTGT GACCGGCGCG GTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT 180
CTGGAGCGGA CTTATTACC AAGCATGGA GGAATATCGT AGGTAAAA ATG CCT ATT 237

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20

																		Met	Pro	Ile	
																		1			
5	GGA	TCC	AAA	GAG	AGG	CCA	ACA	TTT	TTT	GAA	ATT	TTT	AAG	ACA	CGC	TGC					285
	Gly	Ser	Lys	Glu	Arg	Pro	Thr	Phe	Phe	Glu	Ile	Phe	Lys	Thr	Arg	Cys					
	5						10					15									
10	AAC	AAA	GCA	GAT	TTA	GGA	CCA	ATA	AGT	CTT	AAT	TGG	TTT	GAA	GAA	CTT					333
	Asn	Lys	Ala	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Asn	Trp	Phe	Glu	Glu	Leu					
	20					25					30					35					
15	TCT	TCA	GAA	GCT	CCA	CCC	TAT	AAT	TCT	GAA	CCT	GCA	GAA	GAA	TCT	GAA					381
	Ser	Ser	Glu	Ala	Pro	Pro	Tyr	Asn	Ser	Glu	Pro	Ala	Glu	Glu	Ser	Glu					
					40					45					50						
20	CAT	AAA	AAC	AAC	AAT	TAC	GAA	CCA	AAC	CTA	TTT	AAA	ACT	CCA	CAA	AGG					429
	His	Lys	Asn	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr	Pro	Gln	Arg					
				55					60					65							
25	AAA	CCA	TCT	TAT	AAT	CAG	CTG	GCT	TCA	ACT	CCA	ATA	ATA	TTC	AAA	GAG					477
	Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile	Phe	Lys	Glu					
			70				75					80									
30	CAA	GGG	CTG	ACT	CTG	CCG	CTG	TAC	CAA	TCT	CCT	GTA	AAA	GAA	TTA	GAT					525
	Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys	Glu	Leu	Asp					
		85				90					95										
35	AAA	TTC	AAA	TTA	GAC	TTA	GGA	AGG	AAT	GTT	CCC	AAT	AGT	AGA	CAT	AAA					573
	Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser	Arg	His	Lys					
	100				105						110					115					
40	AGT	CTT	CGC	ACA	GTG	AAA	ACT	AAA	ATG	GAT	CAA	GCA	GAT	GAT	GTT	TCC					621
	Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp	Asp	Val	Ser					
					120				125						130						
45	TGT	CCA	CTT	CTA	AAT	TCT	TGT	CTT	AGT	GAA	AGT	CCT	GTT	GTT	CTA	CAA					669
	Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val	Val	Leu	Gln					
				135				140					145								
50	TGT	ACA	CAT	GTA	ACA	CCA	CAA	AGA	GAT	AAG	TCA	GTG	GTA	TGT	GGG	AGT					717
	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val	Cys	Gly	Ser					
			150				155					160									
55	TTG	TTT	CAT	ACA	CCA	AAG	TTT	GTG	AAG	GGT	CGT	CAG	ACA	CCA	AAA	CAT					765
	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr	Pro	Lys	His					
		165				170					175										
60	ATT	TCT	GAA	AGT	CTA	GGA	GCT	GAG	GTG	GAT	CCT	GAT	ATG	TCT	TGG	TCA					813
	Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met	Ser	Trp	Ser					
	180					185					190					195					
65	AGT	TCT	TTA	GCT	ACA	CCA	CCC	ACC	CTT	AGT	TCT	ACT	GTG	CTC	ATA	GTC					861
	Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val	Leu	Ile	Val					
					200				205					210							
70	AGA	AAT	GAA	GAA	GCA	TCT	GAA	ACT	GTA	TTT	CCT	CAT	GAT	ACT	ACT	GCT					909
	Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp	Thr	Thr	Ala					
				215				220					225								
75	AAT	GTG	AAA	AGC	TAT	TTT	TCC	AAT	CAT	GAT	GAA	AGT	CTG	AAG	AAA	AAT					957
	Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu	Lys	Lys	Asn					

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5 GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG 1725
 Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln
 485 490 495

10 GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT 1773
 Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr
 500 505 510 515

15 TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA 1821
 Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys
 520 525 530

20 GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA 1869
 Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser
 535 540 545

25 CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG 1917
 Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp
 550 555 560

30 CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA 1965
 Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu
 565 570 575

35 ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT 2013
 Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His
 580 585 590 595

40 GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA 2061
 Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser
 600 605 610

45 GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA 2109
 Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala
 615 620 625

50 CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG 2157
 Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val
 630 635 640

55 AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA 2205
 Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu
 645 650 655

60 ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA 2253
 Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr
 660 665 670 675

65 TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA 2301
 Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala
 680 685 690

70 AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT 2349
 Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp
 695 700 705

75 TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC 2397
 Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser
 710 715 720

AAA Lys	AAA Lys	GTT Val	TCA Ser	GAT Asp	ATA Ile	AAA Lys	GAA Glu	GAG Glu	GTC Val	TTG Leu	GCT Ala	GCA Ala	GCA Ala	TGT Cys	CAC His	2445
CCA Pro	GTA Val	CAA Gln	CAT His	TCA Ser	AAA Lys	GTG Val	GAA Glu	TAC Tyr	AGT Ser	GAT Asp	ACT Thr	GAC Asp	TTT Phe	CAA Gln	TCC Ser	2493
CAG Gln	AAA Lys	AGT Ser	CTT Leu	TTA Leu	TAT Tyr	GAT Asp	CAT His	GAA Glu	AAT Asn	GCC Ala	AGC Ser	ACT Thr	CTT Leu	ATT Ile	TTA Leu	2541
ACT Thr	CCT Pro	ACT Thr	TCC Ser	AAG Lys	GAT Asp	GTT Val	CTG Leu	TCA Ser	AAC Asn	CTA Leu	GTC Val	ATG Met	ATT Ile	TCT Ser	AGA Arg	2589
GGC Gly	AAA Lys	GAA Glu	TCA Ser	TAC Tyr	AAA Lys	ATG Met	TCA Ser	GAC Asp	AAG Lys	CTC Leu	AAA Lys	GGT Gly	AAC Asn	AAT Asn	TAT Tyr	2637
GAA Glu	TCT Ser	GAT Asp	GTT Val	GAA Glu	TTA Leu	ACC Thr	AAA Lys	AAT Asn	ATT Ile	CCC Pro	ATG Met	GAA Glu	AAG Lys	AAT Asn	CAA Gln	2685
GAT Asp	GTA Val	TGT Cys	GCT Ala	TTA Leu	AAT Asn	GAA Glu	AAT Asn	TAT Tyr	AAA Lys	AAC Asn	GTT Val	GAG Glu	CTG Leu	TTG Leu	CCA Pro	2733
CCT Pro	GAA Glu	AAA Lys	TAC Tyr	ATG Met	AGA Arg	GTA Val	GCA Ala	TCA Ser	CCT Pro	TCA Ser	AGA Arg	AAG Lys	GTA Val	CAA Gln	TTC Phe	2781
AAC Asn	CAA Gln	AAC Asn	ACA Thr	AAT Asn	CTA Leu	ACA Arg	GTA Val	ATC Ile	CAA Gln	AAA Lys	AAT Asn	CAA Gln	GAA Glu	GAA Glu	ACT Thr	2829
ACT Thr	TCA Ser	ATT Ile	TCA Ser	AAA Lys	ATA Ile	ACT Thr	GTC Val	AAT Asn	CCA Pro	GAC Asp	TCT Ser	GAA Glu	GAA Glu	CTT Leu	TTC Phe	2877
TCA Ser	GAC Asp	AAT Asn	GAG Glu	AAT Asn	AAT Asn	TTT Phe	GTC Val	TTC Phe	CAA Gln	GTA Val	GCT Ala	AAT Asn	GAA Glu	AGG Arg	AAT Asn	2925
AAT Asn	CTT Leu	GCT Ala	TTA Leu	GGA Gly	AAT Asn	ACT Thr	AAG Lys	GAA Glu	CTT Leu	CAT His	GAA Glu	ACA Thr	GAC Asp	TTG Leu	ACT Thr	2973
TGT Cys	GTA Val	AAC Asn	GAA Glu	CCC Pro	ATT Ile	TTC Phe	AAG Lys	AAC Asn	TCT Ser	ACC Thr	ATG Met	GTT Val	TTA Leu	TAT Tyr	GGA Gly	3021
GAC Asp	ACA Thr	GGT Gly	GAT Asp	AAA Lys	CAA Gln	GCA Ala	ACC Thr	CAA Gln	GTG Val	TCA Ser	ATT Ile	AAA Lys	AAA Lys	GAT Asp	TTG Leu	3069
GTT Val	TAT Tyr	GTT Val	CTT Leu	GCA Ala	GAG Glu	GAG Glu	AAC Asn	AAA Lys	AAT Asn	AGT Ser	GTA Val	AAG Lys	CAG Gln	CAT His	ATA Ile	3117
AAA	ATG	ACT	CTA	GGT	CAA	GAT	TTA	AAA	TCG	GAC	ATC	TCC	TTG	AAT	ATA	3165

75

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Lys	Met	Thr	Leu	Gly	Gln	Asp	Leu	Lys	Ser	Asp	Ile	Ser	Leu	Asn	Ile		
965						970					975						
GAT	AAA	ATA	CCA	GAA	AAA	AAT	AAT	GAT	TAC	ATG	AAC	AAA	TGG	GCA	GGA	3213	
Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met	Asn	Lys	Trp	Ala	Gly		
980					985					990					995		
CTC	TTA	GGT	CCA	ATT	TCA	AAT	CAC	AGT	TTT	GGA	GGT	AGC	TTG	AGA	ACA	3261	
Leu	Leu	Gly	Pro	Ile	Ser	Asn	His	Ser	Phe	Gly	Gly	Ser	Phe	Arg	Thr		
				1000					1005					1010			
GCT	TCA	AAT	AAG	GAA	ATC	AAG	CTC	TCT	GAA	CAT	AAC	ATT	AAG	AAG	AGC	3309	
Ala	Ser	Asn	Lys	Glu	Ile	Lys	Leu	Ser	Glu	His	Asn	Ile	Lys	Lys	Ser		
			1015					1020					1025				
AAA	ATG	TTC	TTC	AAA	GAT	ATT	GAA	GAA	CAA	TAT	CCT	ACT	AGT	TTA	GCT	3357	
Lys	Met	Phe	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr	Pro	Thr	Ser	Leu	Ala		
		1030					1035					1040					
TGT	GTT	GAA	ATT	GTA	AAT	ACC	TTG	GCA	TTA	GAT	AAT	CAA	AAG	AAA	CTG	3405	
Cys	Val	Glu	Ile	Val	Asn	Thr	Leu	Ala	Leu	Asp	Asn	Gln	Lys	Lys	Leu		
		1045				1050					1055						
AGC	AAG	CCT	CAG	TCA	ATT	AAT	ACT	GTA	TCT	GCA	CAT	TTA	CAG	AGT	AGT	3453	
Ser	Lys	Pro	Gln	Ser	Ile	Asn	Thr	Val	Ser	Ala	His	Leu	Gln	Ser	Ser		
1060					1065					1070				1075			
GTA	GTT	GTT	TCT	GAT	TGT	AAA	AAT	AGT	CAT	ATA	ACC	CCT	CAG	ATG	TTA	3501	
Val	Val	Val	Ser	Asp	Cys	Lys	Asn	Ser	His	Ile	Thr	Pro	Gln	Met	Leu		
				1080					1085					1090			
TTT	TCC	AAG	CAG	GAT	TTT	AAT	TCA	AAC	CAT	AAT	TTA	ACA	CCT	AGC	CAA	3549	
Phe	Ser	Lys	Gln	Asp	Phe	Asn	Ser	Asn	His	Asn	Leu	Thr	Pro	Ser	Gln		
			1095				1100						1105				
AAG	GCA	GAA	ATT	ACA	GAA	CTT	TCT	ACT	ATA	TTA	GAA	GAA	TCA	GGA	AGT	3597	
Lys	Ala	Glu	Ile	Thr	Glu	Leu	Ser	Thr	Ile	Leu	Glu	Glu	Ser	Gly	Ser		
		1110				1115					1120						
CAG	TTT	GAA	TTT	ACT	CAG	TTT	AGA	AAR	CCA	AGC	TAC	ATA	TTG	CAG	AAG	3645	
Gln	Phe	Glu	Phe	Thr	Gln	Phe	Arg	Xaa	Pro	Ser	Tyr	Ile	Leu	Gln	Lys		
		1125				1130					1135						
AGT	ACA	TTT	GAA	GTG	CCT	GAA	AAC	CAG	ATG	ACT	ATC	TTA	AAG	ACC	ACT	3693	
Ser	Thr	Phe	Glu	Val	Pro	Glu	Asn	Gln	Met	Thr	Ile	Leu	Lys	Thr	Thr		
1140					1145					1150				1155			
TCT	GAG	GAA	TGC	AGA	GAT	GCT	GAT	CTT	CAT	GTC	ATA	ATG	AAT	GCC	CCA	3741	
Ser	Glu	Glu	Cys	Arg	Asp	Ala	Asp	Leu	His	Val	Ile	Met	Asn	Ala	Pro		
				1160					1165					1170			
TCG	ATT	GGT	CAG	GTA	GAC	AGC	AGC	AAG	CAA	TTT	GAA	GGT	ACA	GTT	GAA	3789	
Ser	Ile	Gly	Gln	Val	Asp	Ser	Ser	Lys	Gln	Phe	Glu	Gly	Thr	Val	Glu		
			1175					1180					1185				
ATT	AAA	CGG	AAG	TTT	GCT	GGC	CTG	TTG	AAA	AAT	GAC	TGT	AAC	AAA	AGT	3837	
Ile	Lys	Arg	Lys	Phe	Ala	Gly	Leu	Leu	Lys	Asn	Asp	Cys	Asn	Lys	Ser		
		1190				1195					1200						
GCT	TCT	GGT	TAT	TTA	ACA	GAT	GAA	AAT	GAA	GTG	GGG	TTT	AGG	GGC	TTT	3885	
Ala	Ser	Gly	Tyr	Leu	Thr	Asp	Glu	Asn	Glu	Val	Gly	Phe	Arg	Gly	Phe		

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Sub
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	1205	1210	1215	
5	TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln 1220 1225 1230 1235			3933
	AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr 1240 1245 1250			3981
	TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp 1255 1260 1265			4029
	TCT GTC GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val 1270 1275 1280			4077
20	AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu 1285 1290 1295			4125
25	ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg 1300 1305 1310 1315			4173
30	AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser 1320 1325 1330			4221
	CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val 1335 1340 1345			4269
35	TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn 1350 1355 1360			4317
40	ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln 1365 1370 1375			4365
45	ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala 1380 1385 1390 1395			4413
50	CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala 1400 1405 1410			4461
	ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe 1415 1420 1425			4509
55	TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe 1430 1435 1440			4557
60	AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn 1445 1450 1455			4605

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5 TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG 4653
 Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met
 1460 1465 1470 1475

10 GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG 4701
 Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu
 1480 1485 1490

15 AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG 4749
 Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln
 1495 1500 1505

20 GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT 4797
 Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly
 1510 1515 1520

25 TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG 4845
 Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu
 1525 1530 1535

30 GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA 4893
 Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu
 1540 1545 1550 1555

35 ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG 4941
 Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu
 1560 1565 1570

40 GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT 4989
 Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala
 1575 1580 1585

45 GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC 5037
 Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn
 1590 1595 1600

50 CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT 5085
 Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn
 1605 1610 1615

55 TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG 5133
 Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu
 1620 1625 1630 1635

60 AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT 5181
 Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro
 1640 1645 1650

65 GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA 5229
 Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser
 1655 1660 1665

70 GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG 5277
 Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln
 1670 1675 1680

75 ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT 5325
 Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp
 1685 1690 1695

	GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG	5373
	Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu	
	1700 1705 1710 1715	
5	TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT	5421
	Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His	
	1720 1725 1730	
10	CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC	5469
	Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn	
	1735 1740 1745	
15	AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC	5517
	Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu	
	1750 1755 1760	
20	TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT	5565
	Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val	
	1765 1770 1775	
25	GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA	5613
	Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys	
	1780 1785 1790 1795	
30	GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG	5661
	Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu	
	1800 1805 1810	
35	GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT	5709
	Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile	
	1815 1820 1825	
40	AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA	5757
	Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala	
	1830 1835 1840	
45	TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT	5805
	Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile	
	1845 1850 1855	
50	AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG	5853
	Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys	
	1860 1865 1870 1875	
55	GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA	5901
	Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala	
	1880 1885 1890	
60	GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT	5949
	Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser	
	1895 1900 1905	
65	CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC	5997
	Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp	
	1910 1915 1920	
70	ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG	6045
	Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu	
	1925 1930 1935	
75	GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA	6093

	Glu	Lys	Val	Ser	Lys	Ile	Ser	Pro	Cys	Asp	Val	Ser	Leu	Glu	Thr	Ser	
	1940					1945					1950					1955	
5	GAT	ATA	TGT	AAA	TGT	AGT	ATA	GGG	AAG	CTT	CAT	AAG	TCA	GTC	TCA	TCT	6141
	Asp	Ile	Cys	Lys	Cys	Ser	Ile	Gly	Lys	Leu	His	Lys	Ser	Val	Ser	Ser	
					1960					1965					1970		
10	GCA	AAT	ACT	TGT	GGG	ATT	TTT	AGC	ACA	GCA	AGT	GGA	AAA	TCT	GTC	CAG	6189
	Ala	Asn	Thr	Cys	Gly	Ile	Phe	Ser	Thr	Ala	Ser	Gly	Lys	Ser	Val	Gln	
				1975				1980						1985			
15	GTA	TCA	GAT	GCT	TCA	TTA	CAA	AAC	GCA	AGA	CAA	GTG	TTT	TCT	GAA	ATA	6237
	Val	Ser	Asp	Ala	Ser	Leu	Gln	Asn	Ala	Arg	Gln	Val	Phe	Ser	Glu	Ile	
			1990					1995					2000				
20	GAA	GAT	AGT	ACC	AAG	CAA	GTC	TTT	TCC	AAA	GTA	TTG	TTT	AAA	AGT	AAC	6285
	Glu	Asp	Ser	Thr	Lys	Gln	Val	Phe	Ser	Lys	Val	Leu	Phe	Lys	Ser	Asn	
		2005					2010					2015					
25	GAA	CAT	TCA	GAC	CAG	CTC	ACA	AGA	GAA	GAA	AAT	ACT	GCT	ATA	CGT	ACT	6333
	Glu	His	Ser	Asp	Gln	Leu	Thr	Arg	Glu	Glu	Asn	Thr	Ala	Ile	Arg	Thr	
		2020				2025					2030				2035		
30	CCA	GAA	CAT	TTA	ATA	TCC	CAA	AAA	GGC	TTT	TCA	TAT	AAT	GTG	GTA	AAT	6381
	Pro	Glu	His	Leu	Ile	Ser	Gln	Lys	Gly	Phe	Ser	Tyr	Asn	Val	Val	Asn	
					2040					2045					2050		
35	TCA	TCT	GCT	TTC	TCT	GGA	TTT	AGT	ACA	GCA	AGT	GGA	AAG	CAA	GTT	TCC	6429
	Ser	Ser	Ala	Phe	Ser	Gly	Phe	Ser	Thr	Ala	Ser	Gly	Lys	Gln	Val	Ser	
				2055				2060						2065			
40	ATT	TTA	GAA	AGT	TCC	TTA	CAC	AAA	GTT	AAG	GGA	GTG	TTA	GAG	GAA	TTT	6477
	Ile	Leu	Glu	Ser	Ser	Leu	His	Lys	Val	Lys	Gly	Val	Leu	Glu	Glu	Phe	
			2070					2075					2080				
45	GAT	TTA	ATC	AGA	ACT	GAG	CAT	AGT	CTT	CAC	TAT	TCA	CCT	ACG	TCT	AGA	6525
	Asp	Leu	Ile	Arg	Thr	Glu	His	Ser	Leu	His	Tyr	Ser	Pro	Thr	Ser	Arg	
		2085					2090					2095					
50	CAA	AAT	GTA	TCA	AAA	ATA	CTT	CCT	CGT	GTT	GAT	AAG	AGA	AAC	CCA	GAG	6573
	Gln	Asn	Val	Ser	Lys	Ile	Leu	Pro	Arg	Val	Asp	Lys	Arg	Asn	Pro	Glu	
		2100				2105					2110				2115		
55	CAC	TGT	GTA	AAC	TCA	GAA	ATG	GAA	AAA	ACC	TGC	AGT	AAA	GAA	TTT	AAA	6621
	His	Cys	Val	Asn	Ser	Glu	Met	Glu	Lys	Thr	Cys	Ser	Lys	Glu	Phe	Lys	
				2120					2125						2130		
60	TTA	TCA	AAT	AAC	TTA	AAT	GTT	GAA	GGT	GGT	TCT	TCA	GAA	AAT	AAT	CAC	6669
	Leu	Ser	Asn	Asn	Leu	Asn	Val	Glu	Gly	Gly	Ser	Ser	Glu	Asn	Asn	His	
			2135					2140					2145				
65	TCT	ATT	AAA	GTT	TCT	CCA	TAT	CTC	TCT	CAA	TTT	CAA	CAA	GAC	AAA	CAA	6717
	Ser	Ile	Lys	Val	Ser	Pro	Tyr	Leu	Ser	Gln	Phe	Gln	Gln	Asp	Lys	Gln	
		2150						2155					2160				
70	CAG	TTG	GTA	TTA	GGA	ACC	AAA	GTC	TCA	CTT	GTT	GAG	AAC	ATT	CAT	GTT	6765
	Gln	Leu	Val	Leu	Gly	Thr	Lys	Val	Ser	Leu	Val	Glu	Asn	Ile	His	Val	
		2165					2170					2175					
75	TTG	GGA	AAA	GAA	CAG	GCT	TCA	CCT	AAA	AAC	GTA	AAA	ATG	GAA	ATT	GGT	6813
	Leu	Gly	Lys	Glu	Gln	Ala	Ser	Pro	Lys	Asn	Val	Lys	Met	Glu	Ile	Gly	

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Sub
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	2180		2185		2190		2195	
5	AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT							6861
	Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val							
		2200			2205		2210	
	TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA							6909
	Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala							
		2215			2220		2225	
	GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT							6957
	Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser							
		2230			2235		2240	
	AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT							7005
	Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn							
		2245			2250		2255	
20	GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG							7053
	Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu							
		2260			2265		2270	2275
	CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT							7101
25	Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn							
		2280			2285		2290	
	GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA							7149
	Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser							
		2295			2300		2305	
30	AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT							7197
	Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His							
		2310			2315		2320	
35	CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG							7245
	His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys							
		2325			2330		2335	
40	GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA							7293
	Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu							
		2340			2345		2350	2355
	TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT							7341
45	Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser							
		2360			2365		2370	
	TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT							7389
	Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala							
50		2375			2380		2385	
	ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC							7437
	Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr							
		2390			2395		2400	
55	AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT							7485
	Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val							
		2405			2410		2415	
60	GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA							7533
	Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln							
		2420			2425		2430	2435

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	AAC ATT GAT GGA CAT GGC TCT GAT	GAT AGT AAA AAT AAG ATT AAT GAC	7581
5	Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp	2440 2445 2450	
	AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT		7629
	Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala	2455 2460 2465	
10	GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT		7677
	Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser	2470 2475 2480	
15	CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA		7725
	Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln	2485 2490 2495	
20	AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA		7773
	Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr	2500 2505 2510 2515	
	TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT		7821
25	Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val	2520 2525 2530	
	CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA		7869
	Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys	2535 2540 2545	
30	CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC		7917
	His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His	2550 2555 2560	
35	ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA		7965
	Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile	2565 2570 2575	
40	CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT		8013
	Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala	2580 2585 2590 2595	
	GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT		8061
45	Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp	2600 2605 2610	
	CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC		8109
	Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile	2615 2620 2625	
50	ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT		8157
	Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala	2630 2635 2640	
55	AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA		8205
	Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg	2645 2650 2655	
60	TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA		8253
	Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile	2660 2665 2670 2675	

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	ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT	8301
	Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser	
	2680 2685 2690	
5	GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA	8349
	Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys	
	2695 2700 2705	
10	ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT	8397
	Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp	
	2710 2715 2720	
15	GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC	8445
	Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val	
	2725 2730 2735	
20	TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA	8493
	Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly	
	2740 2745 2750 2755	
25	GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA	8541
	Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro	
	2760 2765 2770	
30	GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC	8589
	Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg	
	2775 2780 2785	
35	TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG	8637
	Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu	
	2790 2795 2800	
40	CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT	8685
	Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp	
	2805 2810 2815	
45	GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA	8733
	Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser	
	2820 2825 2830 2835	
50	TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA	8781
	Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala	
	2840 2845 2850	
55	GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT	8829
	Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr	
	2855 2860 2865	
60	AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA	8877
	Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro	
	2870 2875 2880	
65	TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA	8925
	Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln	
	2885 2890 2895	
70	GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT	8973
	Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala	
	2900 2905 2910 2915	
75	TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT	9021

Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn
 2920 2925 2930

5 CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA 9069
 His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu
 2935 2940 2945

10 ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA 9117
 Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser
 2950 2955 2960

15 AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA 9165
 Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys
 2965 2970 2975

20 AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT 9213
 Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp
 2980 2985 2990 2995

TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT 9261
 Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu
 3000 3005 3010

25 GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA 9309
 Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu
 3015 3020 3025

30 GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA 9357
 Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu
 3030 3035 3040

35 ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA 9405
 Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys
 3045 3050 3055

40 TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA 9453
 Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile
 3060 3065 3070 3075

GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC 9501
 Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val
 3080 3085 3090

45 TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA 9549
 Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile
 3095 3100 3105

50 GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC 9597
 Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser
 3110 3115 3120

55 AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT 9645
 Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe
 3125 3130 3135

GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT 9693
 Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe
 3140 3145 3150 3155

60 CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA 9741
 Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile

050644-05233

Sub
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	3160	3165	3170	
5	CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn 3175 3180 3185	9789		
10	GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr 3190 3195 3200	9837		
15	ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser 3205 3210 3215	9885		
20	CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala 3220 3225 3230 3235	9933		
25	AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys 3240 3245 3250	9981		
30	TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys 3255 3260 3265	10029		
35	AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val 3270 3275 3280	10077		
40	AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln 3285 3290 3295	10125		
45	CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys 3300 3305 3310 3315	10173		
50	GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile 3320 3325 3330	10221		
55	TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile 3335 3340 3345	10269		
60	AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile 3350 3355 3360	10317		
	TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr 3365 3370 3375	10365		
	CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu 3380 3385 3390 3395	10413		
	AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr 3400 3405 3410	10461		

ATT ACA ACT AAA AAA TAT ATC TAA
Ile Thr Thr Lys Lys Tyr Ile
3415

10485

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3418 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys
1 5 10 15
Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe
20 25 30
Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu
35 40 45
Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
50 55 60
Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
65 70 75 80
Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
85 90 95
Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
100 105 110
35 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
115 120 125
Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
130 135 140
Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
40 145 150 155 160
Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
165 170 175
Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
180 185 190
45 Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
195 200 205
Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
210 215 220
Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
50 225 230 235 240
Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
245 250 255
Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
260 265 270
55 Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
275 280 285
Asn Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
290 295 300
Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
60 305 310 315 320
Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
325 330 335

000044-052290

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Sub
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Asn	Ala	Asp	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr	
			340					345					350			
Ser	Phe	Val	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser	
		355					360					365				
Asn	Val	Ala	His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser	
		370				375					380					
Lys	Glu	Val	Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu	
	385				390					395					400	
Ser	Gly	Leu	Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile	
			405					410						415		
Ser	Ser	Cys	Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu	
			420					425					430			
Asn	Lys	Arg	Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg	
		435				440						445				
Ile	Ser	Ser	Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val	
	450				455						460					
Val	Asn	Lys	Arg	Asp	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys		
	465				470				475					480		
Ile	Leu	Ala	Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser	
			485						490					495		
Ser	Phe	Gln	Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro	
			500					505					510			
Lys	Glu	Thr	Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn	
		515					520						525			
Phe	Lys	Lys	Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr	
		530				535					540					
Val	Cys	Ser	Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn	
	545				550					555					560	
Gly	Ser	Trp	Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala	Leu	Lys	Asn	
			565						570					575		
Ala	Gly	Leu	Ile	Ser	Thr	Leu	Lys	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr	
			580					585					590			
Ala	Ile	His	Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp	
		595				600						605				
Gln	Lys	Ser	Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu	Ala	Asn	Ala	
		610			615						620					
Phe	Glu	Ala	Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His	
	625				630					635					640	
Ser	Ser	Val	Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr	
			645						650					655		
Leu	Ser	Leu	Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg	
			660					665					670			
Asn	Glu	Thr	Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr	
		675					680					685				
Lys	Glu	Ala	Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro	
		690				695					700					
Glu	Ala	Asp	Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp	
	705				710					715					720	
Pro	Lys	Ser	Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala	
			725						730					735		
Ala	Cys	His	Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp	
			740					745					750			
Phe	Gln	Ser	Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr	
		755						760				765				
Leu	Ile	Leu	Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met	
		770				775						780				
Ile	Ser	Arg	Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly	
		785			790					795					800	
Asn	Asn	Tyr	Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu	
			805						810					815		
Lys	Asn	Gln	Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu	

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			820					825				830		
	Leu	Leu	Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg
			835				840					845		
5	Val	Gln	Phe	Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys
			850				855					860		
	Glu	Glu	Thr	Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp
			865				870					875		
	Glu	Leu	Phe	Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Val
					885							890		
10	Glu	Arg	Asn	Asn	Leu	Ala	Leu	Gly	Asn	Thr	Lys	Glu	Leu	His
					900							905		
	Asp	Leu	Thr	Cys	Val	Asn	Glu	Pro	Ile	Phe	Lys	Asn	Ser	Thr
					915							920		
15	Leu	Tyr	Gly	Asp	Thr	Gly	Asp	Lys	Gln	Ala	Thr	Gln	Val	Ser
												935		
	Lys	Asp	Leu	Val	Tyr	Val	Leu	Ala	Glu	Glu	Asn	Lys	Asn	Ser
												945		
	Gln	His	Ile	Lys	Met	Thr	Leu	Gly	Gln	Asp	Leu	Lys	Ser	Asp
					950							955		
20					965							970		
	Leu	Asn	Ile	Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met
					980							985		
	Trp	Ala	Gly	Leu	Leu	Gly	Pro	Ile	Ser	Asn	His	Ser	Phe	Gly
												990		
25	Phe	Arg	Thr	Ala	Ser	Asn	Lys	Glu	Ile	Lys	Leu	Ser	Glu	His
												1000		
	Lys	Lys	Ser	Lys	Met	Phe	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr
												1005		
	Ser	Leu	Ala	Cys	Val	Glu	Ile	Val	Asn	Thr	Leu	Ala	Leu	Asp
												1010		
30	Lys	Lys	Leu	Ser	Lys	Pro	Gln	Ser	Ile	Asn	Thr	Val	Ser	Ala
												1015		
	Gln	Ser	Ser	Val	Val	Val	Ser	Asp	Cys	Lys	Asn	Ser	His	Ile
												1020		
35	Gln	Met	Leu	Phe	Ser	Lys	Gln	Asp	Phe	Asn	Ser	Asn	His	Asn
												1025		
	Pro	Ser	Gln	Lys	Ala	Glu	Ile	Thr	Glu	Leu	Ser	Thr	Ile	Leu
												1030		
40	Ser	Gly	Ser	Gln	Phe	Glu	Phe	Thr	Gln	Phe	Arg	Xaa	Pro	Ser
												1035		
	Leu	Gln	Lys	Ser	Thr	Phe	Glu	Val	Pro	Glu	Asn	Gln	Met	Thr
												1040		
	Lys	Thr	Thr	Ser	Glu	Glu	Cys	Arg	Asp	Ala	Asp	Leu	His	Val
												1045		
45	Asn	Ala	Pro	Ser	Ile	Gly	Gln	Val	Asp	Ser	Ser	Lys	Gln	Phe
												1050		
	Thr	Val	Glu	Ile	Lys	Arg	Lys	Phe	Ala	Gly	Leu	Leu	Lys	Asn
												1055		
50	Asn	Lys	Ser	Ala	Ser	Gly	Tyr	Leu	Thr	Asp	Glu	Asn	Glu	Val
												1060		
	Arg	Gly	Phe	Tyr	Ser	Ala	His	Gly	Thr	Lys	Leu	Asn	Val	Ser
												1065		
	Ala	Leu	Gln	Lys	Ala	Val	Lys	Leu	Phe	Ser	Asp	Ile	Glu	Asn
												1070		
55	Glu	Glu	Thr	Ser	Ala	Glu	Val	His	Pro	Ile	Ser	Leu	Ser	Ser
												1075		
	Cys	His	Asp	Ser	Val	Val	Ser	Met	Phe	Lys	Ile	Glu	Asn	His
												1080		
	Lys	Thr	Val	Ser	Glu	Lys	Asn	Asn	Lys	Cys	Gln	Leu	Ile	Leu
												1085		
60	Asn	Ile	Glu	Met	Thr	Thr	Gly	Thr	Phe	Val	Glu	Glu	Ile	Thr
												1090		

Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
 1315 1320 1325
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
 1330 1335 1340
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
 1345 1350 1355 136
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
 1365 1370 1375
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
 1380 1385 1390
 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
 1395 1400 1405
 Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
 1410 1415 1420
 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
 1425 1430 1435 144
 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
 1445 1450 1455
 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
 1460 1465 1470
 Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
 1475 1480 1485
 Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
 1490 1495 1500
 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
 1505 1510 1515 152
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
 1525 1530 1535
 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
 1540 1545 1550
 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
 1555 1560 1565
 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
 1570 1575 1580
 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
 1585 1590 1595 160
 Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
 1605 1610 1615
 Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
 1620 1625 1630
 Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
 1635 1640 1645
 Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
 1650 1655 1660
 Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
 1665 1670 1675 168
 Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
 1685 1690 1695
 Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
 1700 1705 1710
 Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
 1715 1720 1725
 Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
 1730 1735 1740
 Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
 1745 1750 1755 176
 Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
 1765 1770 1775
 Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
 1780 1785 1790
 Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile

Sub
A1

0000441 052230

		1795				1800				1805					
		Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn													
		1810				1815				1820					
5		Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly													
		1825				1830				1835					184
		Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His													
						1845				1850					1855
		Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys													
						1860				1865					1870
10		Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys													
						1875				1880					1885
		Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu													
						1890				1895					1900
15		His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val													
						1905				1910					1915
		Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met													192
						1925				1930					1935
		Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu													
20						1940				1945					1950
		Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser													
						1955				1960					1965
		Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys													
						1970				1975					1980
25		Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe													
						1985				1990					1995
		Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe													200
						2005				2010					2015
		Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala													
30						2020				2025					2030
		Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn													
						2035				2040					2045
		Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys													
						2050				2055					2060
35		Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu													
						2065				2070					2075
		Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro													
						2085				2090					2095
		Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg													
40						2100				2105					2110
		Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys													
						2115				2120					2125
		Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu													
						2130				2135					2140
45		Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln													
						2145				2150					2155
		Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn													
						2165				2170					2175
		Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met													
50						2180				2185					2190
		Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn													
						2195				2200					2205
		Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu													
						2210				2215					2220
55		Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu													
						2225				2230					2235
		Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys													
						2245				2250					2255
		Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg													
60						2260				2265					2270
		Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn													
						2275				2280					2285

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sub
a1

5 Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
2290 2295 2300
Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
2305 2310 2315 232
Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
2325 2330 2335
Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
2340 2345 2350
10 Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
2355 2360 2365
Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
2370 2375 2380
Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly
2385 2390 2395 240
Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
2405 2410 2415
His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg
2420 2425 2430
20 Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys
2435 2440 2445
Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln
2450 2455 2460
Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu
2465 2470 2475 248
Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys
2485 2490 2495
Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu
2500 2505 2510
30 Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly
2515 2520 2525
Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly
2530 2535 2540
Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe
2545 2550 2555 256
35 Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly
2565 2570 2575
Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp
2580 2585 2590
40 Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro
2595 2600 2605
Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr
2610 2615 2620
Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys
2625 2630 2635 264
45 Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu
2645 2650 2655
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile
2660 2665 2670
50 Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu
2675 2680 2685
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser
2690 2695 2700
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu
2705 2710 2715 272
55 Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu
2725 2730 2735
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile
2740 2745 2750
60 Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu
2755 2760 2765
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg

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2770 2775 2780
 Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
 2785 2790 2795 2800
 5 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
 2805 2810 2815
 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
 2820 2825 2830
 10 Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu
 2835 2840 2845
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
 2850 2855 2860
 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr
 2865 2870 2875 288
 15 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
 2885 2890 2895
 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
 2900 2905 2910
 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
 2915 2920 2925
 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
 2930 2935 2940
 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln
 2945 2950 2955 296
 25 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
 2965 2970 2975
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
 2980 2985 2990
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
 2995 3000 3005
 30 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
 3010 3015 3020
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
 3025 3030 3035 304
 35 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
 3045 3050 3055
 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
 3060 3065 3070
 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
 3075 3080 3085
 40 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
 3090 3095 3100
 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
 3105 3110 3115 312
 45 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
 3125 3130 3135
 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
 3140 3145 3150
 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
 3155 3160 3165
 50 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
 3170 3175 3180
 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
 3185 3190 3195 320
 55 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
 3205 3210 3215
 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
 3220 3225 3230
 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
 3235 3240 3245
 60 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn
 3250 3255 3260

Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro
 3265 3270 3275 328
 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys
 3285 3290 3295
 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile
 3300 3305 3310
 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe
 3315 3320 3325
 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu
 3330 3335 3340
 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys
 3345 3350 3355 336
 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser
 3365 3370 3375
 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys
 3380 3385 3390
 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys
 3395 3400 3405
 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile
 3410 3415

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC 60
 TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGGGTGCGC GCCGGGAGAA GCGTGAGGGG 120
 ACAGATTGTG GACCGGCGCG GTTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT 180
 CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT 237
 Met Pro Ile
 1
 GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC 285
 Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
 5 10 15
 AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT 333
 Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu
 20 25 30 35
 TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA 381
 Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu
 40 45 50
 CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG 429
 His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg
 55 60 65

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	AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG	477
	Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu	
	70 75 80	
5	CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT	525
	Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp	
	85 90 95	
10	AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA	573
	Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys	
	100 105 110 115	
15	AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC	621
	Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser	
	120 125 130	
20	TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA	669
	Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	
	135 140 145	
25	TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT	717
	Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	
	150 155 160	
30	TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT	765
	Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	
	165 170 175	
35	ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA	813
	Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	
	180 185 190 195	
40	AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC	861
	Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	
	200 205 210	
45	AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT	909
	Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	
	215 220 225	
50	AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT	957
	Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	
	230 235 240	
55	GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA	1005
	Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg	
	245 250 255	
60	GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA	1053
	Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys	
	260 265 270 275	
65	GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA CAT GTC CTA	1101
	Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro His Val Leu	
	280 285 290	
70	GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT	1149
	Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser	
	295 300 305	
75	TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA	1197

	Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu	Gln	Lys	Val	
			310					315					320				
5	AGA	ACT	AGC	AAG	ACT	AGG	AAA	AAA	ATT	TTC	CAT	GAA	GCA	AAC	GCT	GAT	1245
	Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala	Asn	Ala	Asp	
			325				330					335					
	GAA	TGT	GAA	AAA	TCT	AAA	AAC	CAA	GTG	AAA	GAA	AAA	TAC	TCA	TTT	GTA	1293
	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr	Ser	Phe	Val	
			340				345					350				355	
	TCT	GAA	GTG	GAA	CCA	AAT	GAT	ACT	GAT	CCA	TTA	GAT	TCA	AAT	GTA	GCA	1341
	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser	Asn	Val	Ala	
					360					365					370		
	AAT	CAG	AAG	CCC	TTT	GAG	AGT	GGA	AGT	GAC	AAA	ATC	TCC	AAG	GAA	GTT	1389
	Asn	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser	Lys	Glu	Val	
				375					380						385		
	GTA	CCG	TCT	TTG	GCC	TGT	GAA	TGG	TCT	CAA	CTA	ACC	CTT	TCA	GGT	CTA	1437
	Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu	Ser	Gly	Leu	
				390				395						400			
25	AAT	GGA	GCC	CAG	ATG	GAG	AAA	ATA	CCC	CTA	TTG	CAT	ATT	TCT	TCA	TGT	1485
	Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile	Ser	Ser	Cys	
							410					415					
30	GAC	CAA	AAT	ATT	TCA	GAA	AAA	GAC	CTA	TTA	GAC	ACA	GAG	AAC	AAA	AGA	1533
	Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu	Asn	Lys	Arg	
							425					430				435	
	AAG	AAA	GAT	TTT	CTT	ACT	TCA	GAG	AAT	TCT	TTG	CCA	CGT	ATT	TCT	AGC	1581
	Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg	Ile	Ser	Ser	
35					440					445					450		
	CTA	CCA	AAA	TCA	GAG	AAG	CCA	TTA	AAT	GAG	GAA	ACA	GTG	GTA	AAT	AAG	1629
	Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val	Val	Asn	Lys	
					455				460					465			
40	AGA	GAT	GAA	GAG	CAG	CAT	CTT	GAA	TCT	CAT	ACA	GAC	TGC	ATT	CTT	GCA	1677
	Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys	Ile	Leu	Ala	
					470				475				480				
45	GTA	AAG	CAG	GCA	ATA	TCT	GGA	ACT	TCT	CCA	GTG	GCT	TCT	TCA	TTT	CAG	1725
	Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser	Ser	Phe	Gln	
							485					495					
	GGT	ATC	AAA	AAG	TCT	ATA	TTC	AGA	ATA	AGA	GAA	TCA	CCT	AAA	GAG	ACT	1773
	Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro	Lys	Glu	Thr	
50							505					510				515	
	TTC	AAT	GCA	AGT	TTT	TCA	GGT	CAT	ATG	ACT	GAT	CCA	AAC	TTT	AAA	AAA	1821
	Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn	Phe	Lys	Lys	
55					520					525					530		
	GAA	ACT	GAA	GCC	TCT	GAA	AGT	GGA	CTG	GAA	ATA	CAT	ACT	GTT	TGC	TCA	1869
	Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr	Val	Cys	Ser	
					535				540					545			
60	CAG	AAG	GAG	GAC	TCC	TTA	TGT	CCA	AAT	TTA	ATT	GAT	AAT	GGA	AGC	TGG	1917
	Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn	Gly	Ser	Trp	

550 555 560
 5 CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA 1965
 Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu
 565 570 575
 10 ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT 2013
 Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His
 580 585 590 595
 15 GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA 2061
 Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser
 600 605 610
 20 GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA 2109
 Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala
 615 620 625
 25 CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG 2157
 Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val
 630 635 640
 30 AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA 2205
 Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu
 645 650 655
 35 ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA 2253
 Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr
 660 665 670 675
 40 TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA 2301
 Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala
 680 685 690
 45 AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT 2349
 Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp
 695 700 705
 50 TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC 2397
 Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser
 710 715 720
 55 AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC 2445
 Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Cys His
 725 730 735
 60 CCA GTA GAA CAC TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC 2493
 Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser
 740 745 750 755
 65 CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA 2541
 Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu
 760 765 770
 70 ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA 2589
 Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg
 775 780 785
 75 GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT 2637
 Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr
 790 795 800

5	GAA Glu	TCT Ser	GAT Asp	GTT Val	GAA Glu	TTA Leu	ACC Thr	AAA Lys	AAT Asn	ATT Ile	CCC Pro	ATG Met	GAA Glu	AAG Lys	AAT Asn	CAA Gln	2685
	805						810					815					
	GAT Asp	GTA Val	TGT Cys	GCT Ala	TTA Leu	AAT Asn	GAA Glu	AAT Asn	TAT Tyr	AAA Lys	AAC Asn	GTT Val	GAG Glu	CTG Leu	TTG Leu	CCA Pro	2733
	820					825					830					835	
10	CCT Pro	GAA Glu	AAA Lys	TAC Tyr	ATG Met	AGA Arg	GTA Val	GCA Ala	TCA Ser	CCT Pro	TCA Ser	AGA Arg	AAG Lys	GTA Val	CAA Gln	TTC Phe	2781
					840					845					850		
15	AAC Asn	CAA Gln	AAC Asn	ACA Thr	AAT Asn	CTA Leu	AGA Arg	GTA Val	ATC Ile	CAA Gln	AAA Lys	AAT Asn	CAA Gln	GAA Glu	GAA Glu	ACT Thr	2829
				855					860					865			
20	ACT Thr	TCA Ser	ATT Ile	TCA Ser	AAA Lys	ATA Ile	ACT Thr	GTC Val	AAT Asn	CCA Pro	GAC Asp	TCT Ser	GAA Glu	GAA Glu	CTT Leu	TTC Phe	2877
			870					875					880				
25	TCA Ser	GAC Asp	AAT Asn	GAG Glu	AAT Asn	AAT Asn	TTT Phe	GTC Val	TTC Phe	CAA Gln	GTA Val	GCT Ala	AAT Asn	GAA Glu	AGG Arg	AAT Asn	2925
		885					890					895					
30	AAT Asn	CTT Leu	GCT Ala	TTA Leu	GGA Gly	AAT Asn	ACT Thr	AAG Lys	GAA Glu	CTT Leu	CAT His	GAA Glu	ACA Thr	GAC Asp	TTG Leu	ACT Thr	2973
	900					905					910					915	
35	TGT Cys	GTA Val	AAC Asn	GAA Glu	CCC Pro	ATT Ile	TTC Phe	AAG Lys	AAC Asn	TCT Ser	ACC Thr	ATG Met	GTT Val	TTA Leu	TAT Tyr	GGA Gly	3021
					920					925					930		
40	GAC Asp	ACA Thr	GGT Gly	GAT Asp	AAA Lys	CAA Gln	GCA Ala	ACC Thr	CAA Gln	GTG Val	TCA Ser	ATT Ile	AAA Lys	AAA Lys	GAT Asp	TTG Leu	3069
				935					940					945			
45	GTT Val	TAT Tyr	GTT Val	CTT Leu	GCA Ala	GAG Glu	GAG Glu	AAC Asn	AAA Lys	AAT Asn	AGT Ser	GTA Val	AAG Lys	CAG Gln	CAT His	ATA Ile	3117
			950					955					960				
50	AAA Lys	ATG Met	ACT Thr	CTA Leu	GGT Gly	CAA Gln	GAT Asp	TTA Leu	AAA Lys	TCG Ser	GAC Asp	ATC Ile	TCC Ser	TTG Leu	AAT Asn	ATA Ile	3165
		965					970					975					
55	GAT Asp	AAA Lys	ATA Ile	CCA Pro	GAA Glu	AAA Lys	AAT Asn	AAT Asn	GAT Asp	TAC Tyr	ATG Met	GAC Asp	AAA Lys	TGG Trp	GCA Ala	GGA Gly	3213
	980					985					990					995	
60	CTC Leu	TTA Leu	GGT Gly	CCA Pro	ATT Ile	TCA Ser	AAT Asn	CAC His	AGT Ser	TTT Phe	GGA Gly	GGT Gly	AGC Ser	TTC Phe	AGA Arg	ACA Thr	3261
				1000						1005					1010		
65	GCT Ala	TCA Ser	AAT Asn	AAG Lys	GAA Glu	ATC Ile	AAG Lys	CTC Leu	TCT Ser	GAA Glu	CAT His	AAC Asn	ATT Ile	AAG Lys	AAG Lys	AGC Ser	3309
				1015				1020						1025			
70	AAA Lys	ATG Met	TTC Phe	TTC Phe	AAA Lys	GAT Asp	ATT Ile	GAA Glu	GAA Glu	CAA Gln	TAT Tyr	CCT Pro	ACT Thr	AGT Ser	TTA Leu	GCT Ala	3357
			1030					1035					1040				

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Sub
Q1

5	TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu 1045 1050 1055	3405
10	AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser 1060 1065 1070 1075	3453
15	GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu 1080 1085 1090	3501
20	TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln 1095 1100 1105	3549
25	AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser 1110 1115 1120	3597
30	CAG TTT GAA TTT ACT CAG TTT AGA AAG CCA AGC TAC ATA TTG CAG AAG Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys 1125 1130 1135	3645
35	AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr 1140 1145 1150 1155	3693
40	TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro 1160 1165 1170	3741
45	TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu 1175 1180 1185	3789
50	ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser 1190 1195 1200	3837
55	GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe 1205 1210 1215	3885
60	TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln 1220 1225 1230 1235	3933
65	AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr 1240 1245 1250	3981
70	TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp 1255 1260 1265	4029
75	TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val 1270 1275 1280	4077
80	AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA	4125

052250 "T. 2448050"

	Ser	Glu	Lys	Asn	Asn	Lys	Cys	Gln	Leu	Ile	Leu	Gln	Asn	Asn	Ile	Glu	
	1285						1290					1295					
5	ATG	ACT	ACT	GGC	ACT	TTT	GTT	GAA	GAA	ATT	ACT	GAA	AAT	TAC	AAG	AGA	4173
	Met	Thr	Thr	Gly	Thr	Phe	Val	Glu	Glu	Ile	Thr	Glu	Asn	Tyr	Lys	Arg	
	1300					1305					1310					1315	
	AAT	ACT	GAA	AAT	GAA	GAT	AAC	AAA	TAT	ACT	GCT	GCC	AGT	AGA	AAT	TCT	4221
10	Asn	Thr	Glu	Asn	Glu	Asp	Asn	Lys	Tyr	Thr	Ala	Ala	Ser	Arg	Asn	Ser	
					1320					1325					1330		
	CAT	AAC	TTA	GAA	TTT	GAT	GGC	AGT	GAT	TCA	AGT	AAA	AAT	GAT	ACT	GTT	4269
	His	Asn	Leu	Glu	Phe	Asp	Gly	Ser	Asp	Ser	Ser	Lys	Asn	Asp	Thr	Val	
15				1335					1340					1345			
	TGT	ATT	CAT	AAA	GAT	GAA	ACG	GAC	TTG	CTA	TTT	ACT	GAT	CAG	CAC	AAC	4317
	Cys	Ile	His	Lys	Asp	Glu	Thr	Asp	Leu	Leu	Phe	Thr	Asp	Gln	His	Asn	
		1350						1355					1360				
	ATA	TGT	CTT	AAA	TTA	TCT	GGC	CAG	TTT	ATG	AAG	GAG	GGA	AAC	ACT	CAG	4365
	Ile	Cys	Leu	Lys	Leu	Ser	Gly	Gln	Phe	Met	Lys	Glu	Gly	Asn	Thr	Gln	
		1365					1370					1375					
25	ATT	AAA	GAA	GAT	TTG	TCA	GAT	TTA	ACT	TTT	TTG	GAA	GTT	GCG	AAA	GCT	4413
	Ile	Lys	Glu	Asp	Leu	Ser	Asp	Leu	Thr	Phe	Leu	Glu	Val	Ala	Lys	Ala	
	1380					1385					1390					1395	
	CAA	GAA	GCA	TGT	CAT	GGT	AAT	ACT	TCA	AAT	AAA	GAA	CAG	TTA	ACT	GCT	4461
30	Gln	Glu	Ala	Cys	His	Gly	Asn	Thr	Ser	Asn	Lys	Glu	Gln	Leu	Thr	Ala	
					1400					1405					1410		
	ACT	AAA	ACG	GAG	CAA	AAT	ATA	AAA	GAT	TTT	GAG	ACT	TCT	GAT	ACA	TTT	4509
	Thr	Lys	Thr	Glu	Gln	Asn	Ile	Lys	Asp	Phe	Glu	Thr	Ser	Asp	Thr	Phe	
35				1415					1420					1425			
	TTT	CAG	ACT	GCA	AGT	GGG	AAA	AAT	ATT	AGT	GTC	GCC	AAA	GAG	TCA	TTT	4557
	Phe	Gln	Thr	Ala	Ser	Gly	Lys	Asn	Ile	Ser	Val	Ala	Lys	Glu	Ser	Phe	
		1430						1435					1440				
40	AAT	AAA	ATT	GTA	AAT	TTC	TTT	GAT	CAG	AAA	CCA	GAA	GAA	TTG	CAT	AAC	4605
	Asn	Lys	Ile	Val	Asn	Phe	Phe	Asp	Gln	Lys	Pro	Glu	Glu	Leu	His	Asn	
		1445					1450					1455					
45	TTT	TCC	TTA	AAT	TCT	GAA	TTA	CAT	TCT	GAC	ATA	AGA	AAG	AAC	AAA	ATG	4653
	Phe	Ser	Leu	Asn	Ser	Glu	Leu	His	Ser	Asp	Ile	Arg	Lys	Asn	Lys	Met	
	1460					1465					1470				1475		
	GAC	ATT	CTA	AGT	TAT	GAG	GAA	ACA	GAC	ATA	GTT	AAA	CAC	AAA	ATA	CTG	4701
50	Asp	Ile	Leu	Ser	Tyr	Glu	Glu	Thr	Asp	Ile	Val	Lys	His	Lys	Ile	Leu	
					1480					1485					1490		
	AAA	GAA	ACT	GTC	CCA	GTT	GGT	ACT	GGA	AAT	CAA	CTA	GTG	ACC	TTC	CAG	4749
	Lys	Glu	Ser	Val	Pro	Val	Gly	Thr	Gly	Asn	Gln	Leu	Val	Thr	Phe	Gln	
55				1495					1500					1505			
	GGA	CAA	CCC	GAA	CGT	GAT	GAA	AAG	ATC	AAA	GAA	CCT	ACT	CTG	TTG	GGT	4797
	Gly	Gln	Pro	Glu	Arg	Asp	Glu	Lys	Ile	Lys	Glu	Pro	Thr	Leu	Leu	Gly	
		1510						1515					1520				
60	TTT	CAT	ACA	GCT	AGC	GGG	AAA	AAA	GTT	AAA	ATT	GCA	AAG	GAA	TCT	TTG	4845
	Phe	His	Thr	Ala	Ser	Gly	Lys	Lys	Val	Lys	Ile	Ala	Lys	Glu	Ser	Leu	

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	1525		1530		1535																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
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	GAA	GAT	CAA	AAA	AAC	ACT	AGT	TTT	TCC	AAA	GTA	ATA	TCC	AAT	GTA	AAA	
	Glu	Asp	Gln	Lys	Asn	Thr	Ser	Phe	Ser	Lys	Val	Ile	Ser	Asn	Val	Lys	
5	1780					1785					1790					1795	5613
	GAT	GCA	AAT	GCA	TAC	CCA	CAA	ACT	GTA	AAT	GAA	GAT	ATT	TGC	GTT	GAG	5661
	Asp	Ala	Asn	Ala	Tyr	Pro	Gln	Thr	Val	Asn	Glu	Asp	Ile	Cys	Val	Glu	
					1800					1805					1810		
10	GAA	CTT	GTG	ACT	AGC	TCT	TCA	CCC	TGC	AAA	AAT	AAA	AAT	GCA	GCC	ATT	5709
	Glu	Leu	Val	Thr	Ser	Ser	Ser	Pro	Cys	Lys	Asn	Lys	Asn	Ala	Ala	Ile	
				1815					1820					1825			
15	AAA	TTG	TCC	ATA	TCT	AAT	AGT	AAT	AAT	TTT	GAG	GTA	GGG	CCA	CCT	GCA	5757
	Lys	Leu	Ser	Ile	Ser	Asn	Ser	Asn	Asn	Phe	Glu	Val	Gly	Pro	Pro	Ala	
			1830					1835					1840				
20	TTT	AGG	ATA	GCC	AGT	GGT	AAA	ATC	GTT	TGT	GTT	TCA	CAT	GAA	ACA	ATT	5805
	Phe	Arg	Ile	Ala	Ser	Gly	Lys	Ile	Val	Cys	Val	Ser	His	Glu	Thr	Ile	
		1845					1850					1855					
25	AAA	AAA	GTG	AAA	GAC	ATA	TTT	ACA	GAC	AGT	TTC	AGT	AAA	GTA	ATT	AAG	5853
	Lys	Lys	Val	Lys	Asp	Ile	Phe	Thr	Asp	Ser	Phe	Ser	Lys	Val	Ile	Lys	
	1860				1865					1870					1875		
30	GAA	AAC	AAC	GAG	AAT	AAA	TCA	AAA	ATT	TGC	CAA	ACG	AAA	ATT	ATG	GCA	5901
	Glu	Asn	Asn	Glu	Asn	Lys	Ser	Lys	Ile	Cys	Gln	Thr	Lys	Ile	Met	Ala	
				1880					1885					1890			
35	GGT	TGT	TAC	GAG	GCA	TTG	GAT	GAT	TCA	GAG	GAT	ATT	CTT	CAT	AAC	TCT	5949
	Gly	Cys	Tyr	Glu	Ala	Leu	Asp	Asp	Ser	Glu	Asp	Ile	Leu	His	Asn	Ser	
			1895					1900					1905				
40	CTA	GAT	AAT	GAT	GAA	TGT	AGC	ACG	CAT	TCA	CAT	AAG	GTT	TTT	GCT	GAC	5997
	Leu	Asp	Asn	Asp	Glu	Cys	Ser	Thr	His	Ser	His	Lys	Val	Phe	Ala	Asp	
		1910					1915					1920					
45	ATT	CAG	AGT	GAA	GAA	ATT	TTA	CAA	CAT	AAC	CAA	AAT	ATG	TCT	GGA	TTG	6045
	Ile	Gln	Ser	Glu	Glu	Ile	Leu	Gln	His	Asn	Gln	Asn	Met	Ser	Gly	Leu	
		1925					1930				1935						
50	GAG	AAA	GTT	TCT	AAA	ATA	TCA	CCT	TGT	GAT	GTT	AGT	TTG	GAA	ACT	TCA	6093
	Glu	Lys	Val	Ser	Lys	Ile	Ser	Pro	Cys	Asp	Val	Ser	Leu	Glu	Thr	Ser	
	1940				1945					1950					1955		
55	GAT	ATA	TGT	AAA	TGT	AGT	ATA	GGG	AAG	CTT	CAT	AAG	TCA	GTC	TCA	TCT	6141
	Asp	Ile	Cys	Lys	Cys	Ser	Ile	Gly	Lys	Leu	His	Lys	Ser	Val	Ser	Ser	
				1960					1965				1970				
60	GCA	AAT	ACT	TGT	GGG	ATT	TTT	AGC	ACA	GCA	AGT	GGA	AAA	TCT	GTC	CAG	6189
	Ala</																

GAA	CAT	TCA	GAC	CAG	CTC	ACA	AGA	GAA	GAA	AAT	ACT	GCT	ATA	CGT	ACT	6333
Glu	His	Ser	Asp	Gln	Leu	Thr	Arg	Glu	Glu	Asn	Thr	Ala	Ile	Arg	Thr	
2020					2025				2030						2035	
CCA	GAA	CAT	TTA	ATA	TCC	CAA	AAA	GGC	TTT	TCA	TAT	AAT	GTG	GTA	AAT	6381
Pro	Glu	His	Leu	Ile	Ser	Gln	Lys	Gly	Phe	Ser	Tyr	Asn	Val	Val	Asn	
				2040					2045					2050		
TCA	TCT	GCT	TTC	TCT	GGA	TTT	AGT	ACA	GCA	AGT	GGA	AAG	CAA	GTT	TCC	6429
Ser	Ser	Ala	Phe	Ser	Gly	Phe	Ser	Thr	Ala	Ser	Gly	Lys	Gln	Val	Ser	
			2055					2060					2065			
ATT	TTA	GAA	AGT	TCC	TTA	CAC	AAA	GTT	AAG	GGA	GTG	TTA	GAG	GAA	TTT	6477
Ile	Leu	Glu	Ser	Ser	Leu	His	Lys	Val	Lys	Gly	Val	Leu	Glu	Glu	Phe	
		2070					2075					2080				
GAT	TTA	ATC	AGA	ACT	GAG	CAT	AGT	CTT	CAC	TAT	TCA	CCT	ACG	TCT	AGA	6525
Asp	Leu	Ile	Arg	Thr	Glu	His	Ser	Leu	His	Tyr	Ser	Pro	Thr	Ser	Arg	
	2085					2090					2095					
CAA	AAT	GTA	TCA	AAA	ATA	CTT	CCT	CGT	GTT	GAT	AAG	AGA	AAC	CCA	GAG	6573
Gln	Asn	Val	Ser	Lys	Ile	Leu	Pro	Arg	Val	Asp	Lys	Arg	Asn	Pro	Glu	
2100					2105					2110					2115	
CAC	TGT	GTA	AAC	TCA	GAA	ATG	GAA	AAA	ACC	TGC	AGT	AAA	GAA	TTT	AAA	6621
His	Cys	Val	Asn	Ser	Glu	Met	Glu	Lys	Thr	Cys	Ser	Lys	Glu	Phe	Lys	
				2120					2125					2130		
TTA	TCA	AAT	AAC	TTA	AAT	GTT	GAA	GGT	GGT	TCT	TCA	GAA	AAT	AAT	CAC	6669
Leu	Ser	Asn	Asn	Leu	Asn	Val	Glu	Gly	Gly	Ser	Ser	Glu	Asn	Asn	His	
			2135				2140						2145			
TCT	ATT	AAA	GTT	TCT	CCA	TAT	CTC	TCT	CAA	TTT	CAA	CAA	GAC	AAA	CAA	6717
Ser	Ile	Lys	Val	Ser	Pro	Tyr	Leu	Ser	Gln	Phe	Gln	Gln	Asp	Lys	Gln	
		2150					2155					2160				
CAG	TTG	GTA	TTA	GGA	ACC	AAA	GTC	TCA	CTT	GTT	GAG	AAC	ATT	CAT	GTT	6765
Gln	Leu	Val	Leu	Gly	Thr	Lys	Val	Ser	Leu	Val	Glu	Asn	Ile	His	Val	
	2165					2170					2175					
TTG	GGA	AAA	GAA	CAG	GCT	TCA	CCT	AAA	AAC	GTA	AAA	ATG	GAA	ATT	GGT	6813
Leu	Gly	Lys	Glu	Gln	Ala	Ser	Pro	Lys	Asn	Val	Lys	Met	Glu	Ile	Gly	
2180					2185					2190					2195	
AAA	ACT	GAA	ACT	TTT	TCT	GAT	GTT	CCT	GTG	AAA	ACA	AAT	ATA	GAA	GTT	6861
Lys	Thr	Glu	Thr	Phe	Ser	Asp	Val	Pro	Val	Lys	Thr	Asn	Ile	Glu	Val	
				2200					2205				2210			
TGT	TCT	ACT	TAC	TCC	AAA	GAT	TCA	GAA	AAC	TAC	TTT	GAA	ACA	GAA	GCA	6909
Cys	Ser	Thr	Tyr	Ser	Lys	Asp	Ser	Glu	Asn	Tyr	Phe	Glu	Thr	Glu	Ala	
			2215					2220					2225			
GTA	GAA	ATT	GCT	AAA	GCT	TTT	ATG	GAA	GAT	GAT	GAA	CTG	ACA	GAT	TCT	

	Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu	
	2260 2265 2270 2275	
5	CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT	7101
	Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn	
	2280 2285 2290	
10	GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA	7149
	Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser	
	2295 2300 2305	
15	AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT	7197
	Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His	
	2310 2315 2320	
20	CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG	7245
	His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys	
	2325 2330 2335	
25	GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA	7293
	Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu	
	2340 2345 2350 2355	
30	TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT	7341
	Phe Leu Ser Lys Ser His Leu Tyr Gln His Leu Thr Leu Glu Lys Ser	
	2360 2365 2370	
35	TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT	7389
	Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala	
	2375 2380 2385	
40	ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC	7437
	Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr	
	2390 2395 2400	
45	AAA GTC TTT GTT CCA COT TTT AAA ACT AAA TCG CAT TTT CAC AGA GTT	7485
	Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val	
	2405 2410 2415	
50	GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA	7533
	Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln	
	2420 2425 2430 2435	
55	AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC	7581
	Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp	
	2440 2445 2450	
60	AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT	7629
	Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala	
	2455 2460 2465	
65	GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT	7677
	Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser	
	2470 2475 2480	
70	CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA	7725
	Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln	
	2485 2490 2495	
75	AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA	7773
	Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr	

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	Lys	Arg	Lys	Ser	Val	Ser	Thr	Pro	Val	Ser	Ala	Gln	Met	Thr	Ser	Lys	
					3240					3245					3250		
5	TCT	TGT	AAA	GGG	GAG	AAA	GAG	ATT	GAT	GAC	CAA	AAG	AAC	TGC	AAA	AAG	10029
	Ser	Cys	Lys	Gly	Glu	Lys	Glu	Ile	Asp	Asp	Gln	Lys	Asn	Cys	Lys	Lys	
				3255				3260					3265				
10	AGA	AGA	GCC	TTG	GAT	TTC	TTG	AGT	AGA	CTG	CCT	TTA	CCT	CCA	CCT	GTT	10077
	Arg	Arg	Ala	Leu	Asp	Phe	Leu	Ser	Arg	Leu	Pro	Leu	Pro	Pro	Pro	Val	
				3270				3275					3280				
15	AGT	CCC	ATT	TGT	ACA	TTT	GTT	TCT	CCG	GCT	GCA	CAG	AAG	GCA	TTT	CAG	10125
	Ser	Pro	Ile	Cys	Thr	Phe	Val	Ser	Pro	Ala	Ala	Gln	Lys	Ala	Phe	Gln	
				3285				3290					3295				
20	CCA	CCA	AGG	AGT	TGT	GGC	ACC	AAA	TAC	GAA	ACA	CCC	ATA	AAG	AAA	AAA	10173
	Pro	Pro	Arg	Ser	Cys	Gly	Thr	Lys	Tyr	Glu	Thr	Pro	Ile	Lys	Lys	Lys	
						3300		3305			3310					3315	
	GAA	CTG	AAT	TCT	CCT	CAG	ATG	ACT	CCA	TTT	AAA	AAA	TTC	AAT	GAA	ATT	10221
	Glu	Leu	Asn	Ser	Pro	Gln	Met	Thr	Pro	Phe	Lys	Lys	Phe	Asn	Glu	Ile	
						3320				3325					3330		
25	TCT	CTT	TTG	GAA	AGT	AAT	TCA	ATA	GCT	GAC	GAA	GAA	CTT	GCA	TTG	ATA	10269
	Ser	Leu	Leu	Glu	Ser	Asn	Ser	Ile	Ala	Asp	Glu	Glu	Leu	Ala	Leu	Ile	
						3335			3340					3345			
30	AAT	ACC	CAA	GCT	CTT	TTG	TCT	GGT	TCA	ACA	GGA	GAA	AAA	CAA	TTT	ATA	10317
	Asn	Thr	Gln	Ala	Leu	Leu	Ser	Gly	Ser	Thr	Gly	Glu	Lys	Gln	Phe	Ile	
				3350				3355					3360				
35	TCT	GTC	AGT	GAA	TCC	ACT	AGG	ACT	GCT	CCC	ACC	AGT	TCA	GAA	GAT	TAT	10365
	Ser	Val	Ser	Glu	Ser	Thr	Arg	Thr	Ala	Pro	Thr	Ser	Ser	Glu	Asp	Tyr	
				3365				3370					3375				
40	CTC	AGA	CTG	AAA	CGA	CCT	TGT	ACT	ACA	TCT	CTG	ATC	AAA	GAA	CAG	GAG	10413
	Leu	Arg	Leu	Lys	Arg	Arg	Cys	Thr	Thr	Ser	Leu	Ile	Lys	Glu	Gln	Glu	
						3380		3385			3390					3395	
	AGT	TCC	CAG	GCC	AGT	ACG	GAA	GAA	TGT	GAG	AAA	AAT	AAG	CAG	GAC	ACA	10461
	Ser	Ser	Gln	Ala	Ser	Thr	Glu	Glu	Cys	Glu	Lys	Asn	Lys	Gln	Asp	Thr	
						3400				3405					3410		
45	ATT	ACA	ACT	AAA	AAA	TAT	ATC	TAA									10485
	Ile	Thr	Thr	Lys	Lys	Tyr	Ile										
						3415											

50 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3418 amino acids

(B) TYPE: amino acid

55 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Sub
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	Met	Pro	Ile	Gly	Ser	Lys	Glu	Arg	Pro	Thr	Phe	Phe	Glu	Ile	Phe	Lys
	1				5					10					15	
5	Thr	Arg	Cys	Asn	Lys	Ala	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Asn	Trp	Phe
				20					25					30		
	Glu	Glu	Leu	Ser	Ser	Glu	Ala	Pro	Pro	Tyr	Asn	Ser	Glu	Pro	Ala	Glu
			35					40					45			
	Glu	Ser	Glu	His	Lys	Asn	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr
		50				55					60					
10	Pro	Gln	Arg	Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile
	65					70					75					80
	Phe	Lys	Glu	Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys
				85					90						95	
	Glu	Leu	Asp	Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser
				100					105					110		
15	Arg	His	Lys	Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp
			115					120					125			
	Asp	Val	Ser	Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val
		130						135					140			
20	Val	Leu	Gln	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val
	145					150					155					160
	Cys	Gly	Ser	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr
				165						170					175	
25	Pro	Lys	His	Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met
			180						185					190		
	Ser	Trp	Ser	Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val
		195						200					205			
	Leu	Ile	Val	Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp
		210				215						220				
30	Thr	Thr	Ala	Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu
	225					230					235					240
	Lys	Lys	Asn	Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr
				245						250					255	
35	Asn	Gln	Arg	Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn
			260						265					270		
	Ser	Phe	Lys	Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro
		275						280					285			
	His	Val	Leu	Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu
		290				295						300				
40	Glu	Asp	Ser	Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu
		305				310					315					320
	Gln	Lys	Val	Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala
				325						330					335	
45	Asn	Ala	Asp	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr
			340						345					350		
	Ser	Phe	Val	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser
		355						360					365			
	Asn	Val	Ala	Asn	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser
		370				375						380				
50	Lys	Glu	Val	Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu
		385				390					395					400
	Ser	Gly	Leu	Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile
				405						410					415	
55	Ser	Ser	Cys	Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu
			420						425					430		
	Asn	Lys	Arg	Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg
			435					440					445			
	Ile	Ser	Ser	Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val
		450				455						460				
60	Val	Asn	Lys	Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys
		465				470					475					480
	Ile	Leu	Ala	Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser

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5 485 490 495
 Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
 500 505 510
 Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
 515 520 525
 Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
 530 535 540
 Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
 545 550 555 560
 Gly Ser Trp Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
 565 570 575
 Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
 580 585 590
 10 15 20
 Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
 595 600 605
 Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
 610 615 620
 Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His
 625 630 635 640
 Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
 645 650 655
 Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
 660 665 670
 25 Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
 675 680 685
 Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
 690 695 700
 30 Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
 705 710 715 720
 Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
 725 730 735
 Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
 740 745 750
 35 Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
 755 760 765
 Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
 770 775 780
 40 Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
 785 790 795 800
 Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
 805 810 815
 Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
 820 825 830
 45 Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
 835 840 845
 Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
 850 855 860
 50 Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
 865 870 875 880
 Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
 885 890 895
 Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
 900 905 910
 55 Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
 915 920 925
 Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
 930 935 940
 60 Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
 945 950 955 960
 Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
 965 970 975

5 Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys
 980 985 990
 Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
 995 1000 1005
 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
 1010 1015 1020
 Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
 1025 1030 1035 104
 Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
 1045 1050 1055
 Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
 1060 1065 1070
 Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
 1075 1080 1085
 Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
 1090 1095 1100
 Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
 1105 1110 1115 112
 Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
 1125 1130 1135
 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
 1140 1145 1150
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
 1155 1160 1165
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
 1170 1175 1180
 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
 1185 1190 1195 120
 30 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
 1205 1210 1215
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
 1220 1225 1230
 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
 1235 1240 1245
 35 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys
 1250 1255 1260
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
 1265 1270 1275 128
 40 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
 1285 1290 1295
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
 1300 1305 1310
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
 1315 1320 1325
 45 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
 1330 1335 1340
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
 1345 1350 1355 136
 50 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
 1365 1370 1375
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
 1380 1385 1390
 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
 1395 1400 1405
 55 Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
 1410 1415 1420
 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
 1425 1430 1435 144
 60 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
 1445 1450 1455
 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys

1460 1465 1470
 Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
 1475 1480 1485
 5 Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
 1490 1495 1500
 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
 1505 1510 1515 152
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
 1525 1530 1535
 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
 1540 1545 1550
 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
 1555 1560 1565
 15 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
 1570 1575 1580
 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
 1585 1590 1595 160
 Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
 1605 1610 1615
 Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
 1620 1625 1630
 Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
 1635 1640 1645
 25 Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
 1650 1655 1660
 Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
 1665 1670 1675 168
 Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
 1685 1690 1695
 30 Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
 1700 1705 1710
 Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
 1715 1720 1725
 35 Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
 1730 1735 1740
 Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
 1745 1750 1755 176
 Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
 1765 1770 1775
 40 Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
 1780 1785 1790
 Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
 1795 1800 1805
 45 Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn
 1810 1815 1820
 Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly
 1825 1830 1835 184
 Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
 1845 1850 1855
 50 Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
 1860 1865 1870
 Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
 1875 1880 1885
 55 Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
 1890 1895 1900
 His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
 1905 1910 1915 192
 Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
 1925 1930 1935
 60 Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
 1940 1945 1950

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	2435		2440		2445
	Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln				
	2450		2455		2460
5	Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu				
	2465		2470		2475
	Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys				248
		2485		2490	2495
	Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu				
10		2500		2505	2510
	Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly				
		2515		2520	2525
	Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly				
		2530		2535	2540
15	Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe				
		2545		2550	2555
	Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly				
		2565		2570	2575
	Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp				
20		2580		2585	2590
	Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro				
		2595		2600	2605
	Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr				
		2610		2615	2620
25	Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys				
		2625		2630	2635
	Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu				
		2645		2650	2655
	Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile				
30		2660		2665	2670
	Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu				
		2675		2680	2685
	Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser				
		2690		2695	2700
35	Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu				
		2705		2710	2715
	Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu				
		2725		2730	2735
	Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile				
40		2740		2745	2750
	Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu				
		2755		2760	2765
	Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg				
		2770		2775	2780
45	Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro				
		2785		2790	2795
	Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly				
		2805		2810	2815
	Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu				
50		2820		2825	2830
	Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu				
		2835		2840	2845
	Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala				
		2850		2855	2860
55	Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr				
		2865		2870	2875
	Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg				
		2885		2890	2895
	Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala				
60		2900		2905	2910
	Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala				
		2915		2920	2925

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	Leu	Asn	Asn	His	Arg	Gln	Met	Leu	Asn	Asp	Lys	Lys	Gln	Ala	Gln	Ile
	2930						2935						2940			
5	Gln	Leu	Glu	Ile	Arg	Lys	Ala	Met	Glu	Ser	Ala	Glu	Gln	Lys	Glu	Gln
	2945					2950					2955					296
	Gly	Leu	Ser	Arg	Asp	Val	Thr	Thr	Val	Trp	Lys	Leu	Arg	Ile	Val	Ser
					2965					2970					2975	
	Tyr	Ser	Lys	Lys	Glu	Lys	Asp	Ser	Val	Ile	Leu	Ser	Ile	Trp	Arg	Pro
					2980				2985					2990		
10	Ser	Ser	Asp	Leu	Tyr	Ser	Leu	Leu	Thr	Glu	Gly	Lys	Arg	Tyr	Arg	Ile
			2995				3000						3005			
	Tyr	His	Leu	Ala	Thr	Ser	Lys	Ser	Lys	Ser	Lys	Ser	Glu	Arg	Ala	Asn
	3010						3015						3020			
	Ile	Gln	Leu	Ala	Ala	Thr	Lys	Lys	Thr	Gln	Tyr	Gln	Gln	Leu	Pro	Val
15	3025					3030					3035					304
	Ser	Asp	Glu	Ile	Leu	Phe	Gln	Ile	Tyr	Gln	Pro	Arg	Glu	Pro	Leu	His
					3045					3050						3055
	Phe	Ser	Lys	Phe	Leu	Asp	Pro	Asp	Phe	Gln	Pro	Ser	Cys	Ser	Glu	Val
				3060					3065					3070		
20	Asp	Leu	Ile	Gly	Phe	Val	Val	Ser	Val	Val	Lys	Lys	Thr	Gly	Leu	Ala
	3075						3080						3085			
	Pro	Phe	Val	Tyr	Leu	Ser	Asp	Glu	Cys	Tyr	Asn	Leu	Leu	Ala	Ile	Lys
	3090						3095					3100				
	Phe	Trp	Ile	Asp	Leu	Asn	Glu	Asp	Ile	Ile	Lys	Pro	His	Met	Leu	Ile
25	3105					3110					3115					312
	Ala	Ala	Ser	Asn	Leu	Gln	Trp	Arg	Pro	Glu	Ser	Lys	Ser	Gly	Leu	Leu
				3125						3130						3135
	Thr	Leu	Phe	Ala	Gly	Asp	Phe	Ser	Val	Phe	Ser	Ala	Ser	Pro	Lys	Glu
				3140					3145					3150		
30	Gly	His	Phe	Gln	Glu	Thr	Phe	Asn	Lys	Met	Lys	Asn	Thr	Val	Glu	Asn
				3155				3160					3165			
	Ile	Asp	Ile	Leu	Cys	Asn	Glu	Ala	Glu	Asn	Lys	Leu	Met	His	Ile	Leu
	3170					3175					3180					
	His	Ala	Asn	Asp	Pro	Lys	Trp	Ser	Thr	Pro	Thr	Lys	Asp	Cys	Thr	Ser
35	3185					3190					3195					320
	Gly	Pro	Tyr	Thr	Ala	Gln	Ile	Ile	Pro	Gly	Thr	Gly	Asn	Lys	Leu	Leu
				3205						3210						3215
	Met	Ser	Ser	Pro	Asn	Cys	Glu	Ile	Tyr	Tyr	Gln	Ser	Pro	Leu	Ser	Leu
				3220					3225					3230		
40	Cys	Met	Ala	Lys	Arg	Lys	Ser	Val	Ser	Thr	Pro	Val	Ser	Ala	Gln	Met
				3235					3240					3245		
	Thr	Ser	Lys	Ser	Cys	Lys	Gly	Glu	Lys	Glu	Ile	Asp	Asp	Gln	Lys	Asn
				3250					3255					3260		
	Cys	Lys	Lys	Arg	Arg	Ala	Leu	Asp	Phe	Leu	Ser	Arg	Leu	Pro	Leu	Pro
45	3265					3270					3275					328
	Pro	Pro	Val	Ser	Pro	Ile	Cys	Thr	Phe	Val	Ser	Pro	Ala	Ala	Gln	Lys
				3285						3290						3295
	Ala	Phe	Gln	Pro	Pro	Arg	Ser	Cys	Gly	Thr	Lys	Tyr	Glu	Thr	Pro	Ile
				3300					3305					3310		
50	Lys	Lys	Lys	Glu	Leu	Asn	Ser	Pro	Gln	Met	Thr	Pro	Phe	Lys	Lys	Phe
			3315					3320					3325			
	Asn	Glu	Ile	Ser	Leu	Leu	Glu	Ser	Asn	Ser	Ile	Ala	Asp	Glu	Glu	Leu
	3330						3335						3340			
	Ala	Leu	Ile	Asn	Thr	Gln	Ala	Leu	Leu	Ser	Gly	Ser	Thr	Gly	Glu	Lys
55	3345					3350					3355					336
	Gln	Phe	Ile	Ser	Val	Ser	Glu	Ser	Thr	Arg	Thr	Ala	Pro	Thr	Ser	Ser
				3365						3370						3375
	Glu	Asp	Tyr	Leu	Arg	Leu	Lys	Arg	Arg	Cys	Thr	Thr	Ser	Leu	Ile	Lys
				3380					3385					3390		
60	Glu	Gln	Glu	Ser	Ser	Gln	Ala	Ser	Thr	Glu	Glu	Cys	Glu	Lys	Asn	Lys
				3395					3400					3405		
	Gln	Asp	Thr	Ile	Thr	Thr	Lys	Lys	Tyr	Ile						

3410

3415

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 229...10482
 (D) OTHER INFORMATION: BRCA2 (OMI4)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC 60
 TCTGCTGCGC CTCGGGTGTC TTTTGC GGCG GTGGGTGCGC GCCGGGAGAA GCGTGAGGGG 120
 ACAGATTTGT GACCGGCGCG GTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT 180
 CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT 237
 Met Pro Ile
 1

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC 285
 Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
 5 10 15

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT 333
 Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu
 20 25 30 35

TCT TCA GAA GCT CCA CCG TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA 381
 Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu
 40 45 50

CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG 429
 His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg
 55 60 65

AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG 477
 Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu
 70 75 80

CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT 525
 Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp
 85 90 95

AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA 573
 Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys
 100 105 110 115

AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC 621
 Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser
 120 125 130

TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA 669
 Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln
 135 140 145

000441 052230

5 TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT 717
 Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser
 150 155 160

10 TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT 765
 Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His
 165 170 175

15 ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA 813
 Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser
 180 185 190 195

20 AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC 861
 Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val
 200 205 210

25 AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT 909
 Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala
 215 220 225

30 AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT 957
 Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn
 230 235 240

35 GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA 1005
 Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg
 245 250 255

40 GAA GCT GCA AGT CAT GGA TTT GCA AAA ACA TCA GGG AAT TCA TTT AAA 1053
 Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys
 260 265 270 275

45 GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA AAT GTC CTA 1101
 Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro Asn Val Leu
 280 285 290

50 GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT 1149
 Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser
 295 300 305

55 TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA 1197
 Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val
 310 315 320

60 AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT 1245
 Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp
 325 330 335

65 GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA 1293
 Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val
 340 345 350 355

70 TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA 1341
 Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala
 360 365 370

75 CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT 1389
 His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val
 375 380 385

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5
10
15
20

	GTA	CCG	TCT	TTG	GCC	TGT	GAA	TGG	TCT	CAA	CTA	ACC	CTT	TCA	GGT	CTA	1437
	Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu	Ser	Gly	Leu	
			390					395					400				
5	AAT	GGA	GCC	CAG	ATG	GAG	AAA	ATA	CCC	CTA	TTG	CAT	ATT	TCT	TCA	TGT	1485
	Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile	Ser	Ser	Cys	
		405					410					415					
10	GAC	CAA	AAT	ATT	TCA	GAA	AAA	GAC	CTA	TTA	GAC	ACA	GAG	AAC	AAA	AGA	1533
	Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu	Asn	Lys	Arg	
		420					425					430				435	
15	AAG	AAA	GAT	TTT	CTT	ACT	TCA	GAG	AAT	TCT	TTG	CCA	CGT	ATT	TCT	AGC	1581
	Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg	Ile	Ser	Ser	
					440					445					450		
20	CTA	CCA	AAA	TCA	GAG	AAG	CCA	TTA	AAT	GAG	GAA	ACA	GTG	GTA	AAT	AAG	1629
	Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val	Val	Asn	Lys	
					455				460					465			
25	AGA	GAT	GAA	GAG	CAG	CAT	CTT	GAA	TCT	CAT	ACA	GAC	TGC	ATT	CTT	GCA	1677
	Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys	Ile	Leu	Ala	
			470						475				480				
30	GTA	AAG	CAG	GCA	ATA	TCT	GGA	ACT	TCT	CCA	GTG	GCT	TCT	TCA	TTT	CAG	1725
	Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser	Ser	Phe	Gln	
			485				490					495					
35	GGT	ATC	AAA	AAG	TCT	ATA	TTC	AGA	ATA	AGA	GAA	TCA	CCT	AAA	GAG	ACT	1773
	Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro	Lys	Glu	Thr	
		500				505					510				515		
40	TTC	AAT	GCA	AGT	TTT	TCA	GGT	CAT	ATG	ACT	GAT	CCA	AAC	TTT	AAA	AAA	1821
	Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn	Phe	Lys	Lys	
					520				525						530		
45	GAA	ACT	GAA	GCC	TCT	GAA	AGT	GGA	CTG	GAA	ATA	CAT	ACT	GTT	TGC	TCA	1869
	Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr	Val	Cys	Ser	
				535					540					545			
50	CAG	AAG	GAG	GAC	TCC	TTA	TGT	CCA	AAT	TTA	ATT	GAT	AAT	GGA	AGC	TGG	1917
	Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn	Gly	Ser	Trp	
			550					555					560				
55	CCA	GCC	ACC	ACC	ACA	CAG	AAT	TCT	GTA	GCT	TTG	AAG	AAT	GCA	GGT	TTA	1965
	Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala	Leu	Lys	Asn	Ala	Gly	Leu	
			565				570					575					
60	ATA	TCC	ACT	TTG	AAA	AAG	AAA	ACA	AAT	AAG	TTT	ATT	TAT	GCT	ATA	CAT	2013
	Ile	Ser	Thr	Leu	Lys	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr	Ala	Ile	His	
						585					590				595		
65	GAT	GAA	ACA	TCT	TAT	AAA	GGA	AAA	AAA	ATA	CCG	AAA	GAC	CAA	AAA	TCA	2061
	Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp	Gln	Lys	Ser	
					600					605					610		
70	GAA	CTA	ATT	AAC	TGT	TCA	GCC	CAG	TTT	GAA	GCA	AAT	GCT	TTT	GAA	GCA	2109
	Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu	Ala	Asn	Ala	Phe	Glu	Ala	
				615				620						625			
75	CCA	CTT	ACA	TTT	GCA	AAT	GCT	GAT	TCA	GGT	TTA	TTG	CAT	TCT	TCT	GTG	2157

	Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His	Ser	Ser	Val	
			630					635					640				
5	AAA	AGA	AGC	TGT	TCA	CAG	AAT	GAT	TCT	GAA	GAA	CCA	ACT	TTG	TCC	TTA	2205
	Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr	Leu	Ser	Leu	
		645					650					655					
10	ACT	AGC	TCT	TTT	GGG	ACA	ATT	CTG	AGG	AAA	TGT	TCT	AGA	AAT	GAA	ACA	2253
	Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg	Asn	Glu	Thr	
		660				665					670					675	
	TGT	TCT	AAT	AAT	ACA	GTA	ATC	TCT	CAG	GAT	CTT	GAT	TAT	AAA	GAA	GCA	2301
	Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr	Lys	Glu	Ala	
					680					685					690		
	AAA	TGT	AAT	AAG	GAA	AAA	CTA	CAG	TTA	TTT	ATT	ACC	CCA	GAA	GCT	GAT	2349
	Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro	Glu	Ala	Asp	
				695					700					705			
20	TCT	CTG	TCA	TGC	CTG	CAG	GAA	GGA	CAG	TGT	GAA	AAT	GAT	CCA	AAA	AGC	2397
	Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp	Pro	Lys	Ser	
			710					715					720				
25	AAA	AAA	GTT	TCA	GAT	ATA	AAA	GAA	GAG	GTC	TTG	GCT	GCA	GCA	TGT	CAC	2445
	Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala	Ala	Cys	His	
			725				730				735						
30	CCA	GTA	CAA	CAT	TCA	AAA	GTG	GAA	TAC	AGT	GAT	ACT	GAC	TTT	CAA	TCC	2493
	Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp	Phe	Gln	Ser	
						745					750					755	
	CAG	AAA	AGT	CTT	TTA	TAT	GAT	CAT	GAA	AAT	GCC	AGC	ACT	CTT	ATT	TTA	2541
	Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr	Leu	Ile	Leu	
					760					765					770		
35	ACT	CCT	ACT	TCC	AAG	GAT	GTT	CTG	TCA	AAC	CTA	GTC	ATG	ATT	TCT	AGA	2589
	Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met	Ile	Ser	Arg	
				775					780					785			
40	GGC	AAA	GAA	TCA	TAC	AAA	ATG	TCA	GAC	AAG	CTC	AAA	GGT	AAC	AAT	TAT	2637
	Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly	Asn	Asn	Tyr	
			790					795					800				
45	GAA	TCT	GAT	GTT	GAA	TTA	ACC	AAA	AAT	ATT	CCC	ATG	GAA	AAG	AAT	CAA	2685
	Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu	Lys	Asn	Gln	
			805				810					815					
50	GAT	GTA	TGT	GCT	TTA	AAT	GAA	AAT	TAT	AAA	AAC	GTT	GAG	CTG	TTG	CCA	2733
	Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu	Leu	Leu	Pro	
						825					830					835	
	CCT	GAA	AAA	TAC	ATG	AGA	GTA	GCA	TCA	CCT	TCA	AGA	AAG	GTA	CAA	TTC	2781
	Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys	Val	Gln	Phe	
					840						845				850		
55	AAC	CAA	AAC	ACA	AAT	CTA	AGA	GTA	ATC	CAA	AAA	AAT	CAA	GAA	GAA	ACT	2829
	Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln	Glu	Glu	Thr	
				855					860					865			
60	ACT	TCA	ATT	TCA	AAA	ATA	ACT	GTC	AAT	CCA	GAC	TCT	GAA	GAA	CTT	TTC	2877
	Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu	Glu	Leu	Phe	

0908441 0523
 062250 1443060
 sub
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090844Z 052200

Sub
a1

	870	875	880	
5	TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn 885 890 895			2925
10	AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr 900 905 910 915			2973
15	TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly 920 925 930			3021
20	GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu 935 940 945			3069
25	GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile 950 955 960			3117
30	AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile 965 970 975			3165
35	GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG AAC AAA TGG GCA GGA Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly 980 985 990 995			3213
40	CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr 1000 1005 1010			3261
45	GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser 1015 1020 1025			3309
50	AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala 1030 1035 1040			3357
55	TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu 1045 1050 1055			3405
60	AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser 1060 1065 1070 1075			3453
65	GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu 1080 1085 1090			3501
70	TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln 1095 1100 1105			3549
75	AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser 1110 1115 1120			3597

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5	CAG TTT GAA TTT ACT CAG TTT AGA AAG CCA AGC TAC ATA TTG CAG AAG Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys	3645
	1125 1130 1135	
10	AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr	3693
	1140 1145 1150 1155	
15	TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro	3741
	1160 1165 1170	
20	TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu	3789
	1175 1180 1185	
25	ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser	3837
	1190 1195 1200	
30	GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe	3885
	1205 1210 1215	
35	TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln	3933
	1220 1225 1230 1235	
40	AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr	3981
	1240 1245 1250	
45	TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp	4029
	1255 1260 1265	
50	TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val	4077
	1270 1275 1280	
55	AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu	4125
	1285 1290 1295	
60	ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg	4173
	1300 1305 1310 1315	
65	AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser	4221
	1320 1325 1330	
70	CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val	4269
	1335 1340 1345	
75	TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn	4317
	1350 1355 1360	

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Sub
A1

5	ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln 1365 1370 1375	4365
10	ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala 1380 1385 1390 1395	4413
15	CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala 1400 1405 1410	4461
20	ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe 1415 1420 1425	4509
25	TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe 1430 1435 1440	4557
30	AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn 1445 1450 1455	4605
35	TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met 1460 1465 1470 1475	4653
40	GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu 1480 1485 1490	4701
45	AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln 1495 1500 1505	4749
50	GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly 1510 1515 1520	4797
55	TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu 1525 1530 1535	4845
60	GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu 1540 1545 1550 1555	4893
65	ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu 1560 1565 1570	4941
70	GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala 1575 1580 1585	4989
75	GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn 1590 1595 1600	5037
80	CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT	5085

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	Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn	
	1605 1610 1615	
5	TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG 5133 Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu 1620 1625 1630 1635	
10	AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT 5181 Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro 1640 1645 1650	
15	GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA 5229 Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser 1655 1660 1665	
20	GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG 5277 Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln 1670 1675 1680	
25	ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT 5325 Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp 1685 1690 1695	
30	GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG 5373 Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu 1700 1705 1710 1715	
35	TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT 5421 Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His 1720 1725 1730	
40	CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC 5469 Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn 1735 1740 1745	
45	AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC 5517 Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu 1750 1755 1760	
50	TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT 5565 Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val 1765 1770 1775	
55	GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA 5613 Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys 1780 1785 1790 1795	
60	GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG 5661 Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu 1800 1805 1810	
	GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT 5709 Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile 1815 1820 1825	
	AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA 5757 Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala 1830 1835 1840	
	TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT 5805 Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile	

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Sub
a

	1845	1850	1855	
5	AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys 1860 1865 1870 1875	5853		
10	GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala 1880 1885 1890	5901		
15	GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser 1895 1900 1905	5949		
20	CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp 1910 1915 1920	5997		
25	ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu 1925 1930 1935	6045		
30	GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser 1940 1945 1950 1955	6093		
35	GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser 1960 1965 1970	6141		
40	GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln 1975 1980 1985	6189		
45	GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile 1990 1995 2000	6237		
50	GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn 2005 2010 2015	6285		
55	GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr 2020 2025 2030 2035	6333		
60	CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn 2040 2045 2050	6381		
65	TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser 2055 2060 2065	6429		
70	ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe 2070 2075 2080	6477		
75	GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg 2085 2090 2095	6525		

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Sub

Al

5	CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu	6573
	2100 2105 2110 2115	
	CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys	6621
	2120 2125 2130	
10	TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His	6669
	2135 2140 2145	
15	TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln	6717
	2150 2155 2160	
20	CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val	6765
	2165 2170 2175	
25	TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly	6813
	2180 2185 2190 2195	
	AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val	6861
	2200 2205 2210	
30	TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala	6909
	2215 2220 2225	
35	GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser	6957
	2230 2235 2240	
40	AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn	7005
	2245 2250 2255	
45	GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu	7053
	2260 2265 2270 2275	
	CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn	7101
	2280 2285 2290	
50	GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser	7149
	2295 2300 2305	
55	AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His	7197
	2310 2315 2320	
60	CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys	7245
	2325 2330 2335	

Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala
 2580 2585 2590 2595

5 GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT 8061
 Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp
 2600 2605 2610

10 CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC 8109
 Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile
 2615 2620 2625

15 ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT 8157
 Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala
 2630 2635 2640

AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA 8205
 Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg
 2645 2650 2655

20 TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA 8253
 Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile
 2660 2665 2670 2675

25 ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT 8301
 Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser
 2680 2685 2690

30 GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA 8349
 Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys
 2695 2700 2705

ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT 8397
 Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp
 2710 2715 2720

35 GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC 8445
 Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val
 2725 2730 2735

40 TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA 8493
 Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly
 2740 2745 2750 2755

45 GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA 8541
 Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro
 2760 2765 2770

50 GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC 8589
 Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg
 2775 2780 2785

55 TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG 8637
 Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu
 2790 2795 2800

CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT 8685
 Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp
 2805 2810 2815

60 GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA 8733
 Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser

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sub
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	2820	2825	2830	2835	
5	TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA	8781			
	Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala				
	2840 2845 2850				
10	GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT	8829			
	Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr				
	2855 2860 2865				
15	AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA	8877			
	Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro				
	2870 2875 2880				
20	TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA	8925			
	Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln				
	2885 2890 2895				
25	GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT	8973			
	Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala				
	2900 2905 2910 2915				
30	TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT	9021			
	Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn				
	2920 2925 2930				
35	CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA	9069			
	His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu				
	2935 2940 2945				
40	ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA	9117			
	Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser				
	2950 2955 2960				
45	AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA	9165			
	Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys				
	2965 2970 2975				
50	AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT	9213			
	Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp				
	2980 2985 2990 2995				
55	TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT	9261			
	Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu				
	3000 3005 3010				
60	GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA	9309			
	Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu				
	3015 3020 3025				
65	GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA	9357			
	Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu				
	3030 3035 3040				
70	ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA	9405			
	Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys				
	3045 3050 3055				
75	TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA	9453			
	Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile				
	3060 3065 3070 3075				

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5	GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC	9501
	Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val	
	3080 3085 3090	
10	TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA	9549
	Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile	
	3095 3100 3105	
15	GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC	9597
	Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser	
	3110 3115 3120	
20	AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT	9645
	Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe	
	3125 3130 3135	
25	GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT	9693
	Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe	
	3140 3145 3150 3155	
30	CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA	9741
	Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile	
	3160 3165 3170	
35	CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT	9789
	Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn	
	3175 3180 3185	
40	GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC	9837
	Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr	
	3190 3195 3200	
45	ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT	9885
	Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser	
	3205 3210 3215	
50	CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC	9933
	Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala	
	3220 3225 3230 3235	
55	AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG	9981
	Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys	
	3240 3245 3250	
60	TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG	10029
	Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys	
	3255 3260 3265	
65	AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT	10077
	Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val	
	3270 3275 3280	
70	AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG	10125
	Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln	
	3285 3290 3295	
75	CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA	10173
	Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys	
	3300 3305 3310 3315	

GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT 10221
Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile
3320 3325 3330

5

TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA 10269
Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile
3335 3340 3345

10

AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA 10317
Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile
3350 3355 3360

15

TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT 10365
Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr
3365 3370 3375

20

CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413
Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu
3380 3385 3390 3395

25

AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461
Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr
3400 3405 3410

30

ATT ACA ACT AAA AAA TAT ATC TAA 10485
Ile Thr Thr Lys Lys Tyr Ile
3415

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys
1 5 10 15
Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe
20 25 30
Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu
35 40 45
Glu Ser Glu His Lys Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
50 55 60
Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
65 70 75 80
Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
85 90 95
Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
100 105 110
Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
115 120 125
Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
130 135 140
Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val

Sub
a

	145				150				155			160
	Cys	Gly	Ser	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys
					165				170			Gln
5	Pro	Lys	His	Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val
				180					185			175
	Ser	Trp	Ser	Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu
			195					200				205
10	Leu	Ile	Val	Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val
		210					215					220
	Thr	Thr	Ala	Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His
		225				230					235	
	Lys	Lys	Asn	Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp
					245					250		255
15	Asn	Gln	Arg	Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys
					260				265			
	Ser	Phe	Lys	Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly
			275					280				285
	Asn	Val	Leu	Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val
		290					295					300
20	Glu	Asp	Ser	Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg
		305				310					315	
	Gln	Lys	Val	Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile
					325					330		335
25	Asn	Ala	Asp	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val
					340				345			350
	Ser	Phe	Val	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp
			355					360				365
	Asn	Val	Ala	His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser
		370					375					380
30	Lys	Glu	Val	Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser
		385				390					395	
	Ser	Gly	Leu	Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro
					405					410		415
35	Ser	Ser	Cys	Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu
					420				425			430
	Asn	Lys	Arg	Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn
			435				440					445
	Ile	Ser	Ser	Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn
		450					455				460	
40	Val	Asn	Lys	Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser
		465				470				475		480
	Ile	Leu	Ala	Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser
					485				490			495
45	Ser	Phe	Gln	Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile
					500				505			510
	Lys	Glu	Thr	Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met
			515				520					525
	Phe	Lys	Lys	Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu
		530					535					540
50	Val	Cys	Ser	Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn
		545				550				555		560
	Gly	Ser	Trp	Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val
					565				570			575
55	Ala	Gly	Leu	Ile	Ser	Thr	Leu	Lys	Lys	Lys	Thr	Asn
					580				585			590
	Ala	Ile	His	Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys
			595				600					605
	Gln	Lys	Ser	Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe
		610					615					620
60	Phe	Glu	Ala	Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser
		625				630				635		640

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	Ser	Ser	Val	Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr
					645					650					655	
5	Leu	Ser	Leu	Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg
				660					665					670		
	Asn	Glu	Thr	Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr
				675				680					685			
	Lys	Glu	Ala	Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro
				690			695					700				
10	Glu	Ala	Asp	Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp
	705					710					715					720
	Pro	Lys	Ser	Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala
					725					730					735	
	Ala	Cys	His	Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp
15					740				745					750		
	Phe	Gln	Ser	Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr
					755			760				765				
	Leu	Ile	Leu	Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met
					770			775				780				
20	Ile	Ser	Arg	Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly
	785					790					795					800
	Asn	Asn	Tyr	Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu
					805					810					815	
25	Lys	Asn	Gln	Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu
				820					825					830		
	Leu	Leu	Pro	Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys
				835				840					845			
	Val	Gln	Phe	Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln
				850			855					860				
30	Glu	Glu	Thr	Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu
	865					870					875					880
	Glu	Leu	Phe	Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Val	Ala	Asn
					885					890					895	
	Glu	Arg	Asn	Asn	Leu	Ala	Leu	Gly	Asn	Thr	Lys	Glu	Leu	His	Glu	Thr
35					900				905					910		
	Asp	Leu	Thr	Cys	Val	Asn	Glu	Pro	Ile	Phe	Lys	Asn	Ser	Thr	Met	Val
				915				920					925			
	Leu	Tyr	Gly	Asp	Thr	Gly	Asp	Lys	Gln	Ala	Thr	Gln	Val	Ser	Ile	Lys
				930			935					940				
40	Lys	Asp	Leu	Val	Tyr	Val	Leu	Ala	Glu	Glu	Asn	Lys	Asn	Ser	Val	Lys
						950				955					960	
	Gln	His	Ile	Lys	Met	Thr	Leu	Gly	Gln	Asp	Leu	Lys	Ser	Asp	Ile	Ser
					965					970					975	
	Leu	Asn	Ile	Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met	Asn	Lys
45				980					985					990		
	Trp	Ala	Gly	Leu	Leu	Gly	Pro	Ile	Ser	Asn	His	Ser	Phe	Gly	Gly	Ser
				995				1000					1005			
	Phe	Arg	Thr	Ala	Ser	Asn	Lys	Glu	Ile	Lys	Leu	Ser	Glu	His	Asn	Ile
				1010				1015				1020				
50	Lys	Lys	Ser	Lys	Met	Phe	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr	Pro	Thr
						1030					1035				104	
	Ser	Leu	Ala	Cys	Val	Glu	Ile	Val	Asn	Thr	Leu	Ala	Leu	Asp	Asn	Gln
					1045					1050					1055	
	Lys	Lys	Leu	Ser	Lys	Pro	Gln	Ser	Ile	Asn	Thr	Val	Ser	Ala	His	Leu
55					1060				1065					1070		
	Gln	Ser	Ser	Val	Val	Val	Ser	Asp	Cys	Lys	Asn	Ser	His	Ile	Thr	Pro
					1075				1080				1085			
	Gln	Met	Leu	Phe	Ser	Lys	Gln	Asp	Phe	Asn	Ser	Asn	His	Asn	Leu	Thr
					1090			1095				1100				
60	Pro	Ser	Gln	Lys	Ala	Glu	Ile	Thr	Glu	Leu	Ser	Thr	Ile	Leu	Glu	Glu
						1105		1110				1115			112	
	Ser	Gly	Ser	Gln	Phe	Glu	Phe	Thr	Gln	Phe	Arg	Lys	Pro	Ser	Tyr	Ile

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5 1125 1130 1135
 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
 1140 1145 1150
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
 1155 1160 1165
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
 1170 1175 1180
 10 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
 1185 1190 1195 120
 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
 1205 1210 1215
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
 1220 1225 1230
 15 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
 1235 1240 1245
 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys
 1250 1255 1260
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
 1265 1270 1275 128
 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
 1285 1290 1295
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
 1300 1305 1310
 25 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
 1315 1320 1325
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
 1330 1335 1340
 30 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
 1345 1350 1355 136
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
 1365 1370 1375
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
 1380 1385 1390
 35 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
 1395 1400 1405
 Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
 1410 1415 1420
 40 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
 1425 1430 1435 144
 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
 1445 1450 1455
 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
 1460 1465 1470
 45 Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
 1475 1480 1485
 Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
 1490 1495 1500
 50 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
 1505 1510 1515 152
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
 1525 1530 1535
 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
 1540 1545 1550
 55 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
 1555 1560 1565
 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
 1570 1575 1580
 60 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
 1585 1590 1595 160
 Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
 1605 1610 1615

5	10	15	20	25	30	35	40	45	50	55	60					
	Ser	Asp	Asn	Leu	Cys	Arg	Gln	Thr	Glu	Asn	Leu	Lys	Thr	Ser	Lys	Ser
				1620					1625					1630		
	Ile	Phe	Leu	Lys	Val	Lys	Val	His	Glu	Asn	Val	Glu	Lys	Glu	Thr	Ala
				1635					1640					1645		
	Lys	Ser	Pro	Ala	Thr	Cys	Tyr	Thr	Asn	Gln	Ser	Pro	Tyr	Ser	Val	Ile
				1650					1655					1660		
	Glu	Asn	Ser	Ala	Leu	Ala	Phe	Tyr	Thr	Ser	Cys	Ser	Arg	Lys	Thr	Ser
									1670					1675		168
	Val	Ser	Gln	Thr	Ser	Leu	Leu	Glu	Ala	Lys	Lys	Trp	Leu	Arg	Glu	Gly
																1695
	Ile	Phe	Asp	Gly	Gln	Pro	Glu	Arg	Ile	Asn	Thr	Ala	Asp	Tyr	Val	Gly
				1700										1710		
	Asn	Tyr	Leu	Tyr	Glu	Asn	Asn	Ser	Asn	Ser	Thr	Ile	Ala	Glu	Asn	Asp
				1715										1725		
	Lys	Asn	His	Leu	Ser	Glu	Lys	Gln	Asp	Thr	Tyr	Leu	Ser	Asn	Ser	Ser
				1730										1740		
	Met	Ser	Asn	Ser	Tyr	Ser	Tyr	His	Ser	Asp	Glu	Val	Tyr	Asn	Asp	Ser
																176
	Gly	Tyr	Leu	Ser	Lys	Asn	Lys	Leu	Asp	Ser	Gly	Ile	Glu	Pro	Val	Leu
																1775
	Lys	Asn	Val	Glu	Asp	Gln	Lys	Asn	Thr	Ser	Phe	Ser	Lys	Val	Ile	Ser
																1790
	Asn	Val	Lys	Asp	Ala	Asn	Ala	Tyr	Pro	Gln	Thr	Val	Asn	Glu	Asp	Ile
																1805
	Cys	Val	Glu	Glu	Leu	Val	Thr	Ser	Ser	Ser	Pro	Cys	Lys	Asn	Lys	Asn
																1820
	Ala	Ala	Ile	Lys	Leu	Ser	Ile	Ser	Asn	Ser	Asn	Asn	Phe	Glu	Val	Gly
																184
	Pro	Pro	Ala	Phe	Arg	Ile	Ala	Ser	Gly	Lys	Ile	Val	Cys	Val	Ser	His
																1855
	Glu	Thr	Ile	Lys	Lys	Val	Lys	Asp	Ile	Phe	Thr	Asp	Ser	Phe	Ser	Lys
																1870
	Val	Ile	Lys	Glu	Asn	Asn	Glu	Asn	Lys	Ser	Lys	Ile	Cys	Gln	Thr	Lys
																1885
	Ile	Met	Ala	Gly	Cys	Tyr	Glu	Ala	Leu	Asp	Asp	Ser				

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5 2100 2105 2110
 2115 2120 2125
 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
 2130 2135 2140
 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
 2145 2150 2155 216
 Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
 2165 2170 2175
 Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
 2180 2185 2190
 Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
 2195 2200 2205
 10 2210 2215 2220
 Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
 15 2225 2230 2235
 Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
 20 2245 2250 2255
 Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
 2260 2265 2270
 Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
 2275 2280 2285
 Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
 25 2290 2295 2300
 Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
 2305 2310 2315 232
 Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
 2325 2330 2335
 Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
 30 2340 2345 2350
 Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
 2355 2360 2365
 Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
 35 2370 2375 2380
 Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
 2385 2390 2395 240
 Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly
 40 2405 2410 2415
 Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
 2420 2425 2430
 His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg
 2435 2440 2445
 Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys
 45 2450 2455 2460
 Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln
 2465 2470 2475 248
 Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu
 2485 2490 2495
 Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys
 50 2500 2505 2510
 Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu
 2515 2520 2525
 Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly
 55 2530 2535 2540
 Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly
 2545 2550 2555 256
 Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe
 2565 2570 2575
 Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly
 60 2580 2585 2590
 Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp

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	Gly	Lys	Ala	Gly	Lys	Glu	Glu	Phe	Tyr	Arg	Ala	Leu	Cys	Asp	Thr	Pro	2595	2600	2605
5	Gly	Val	Asp	Pro	Lys	Leu	Ile	Ser	Arg	Ile	Trp	Val	Tyr	Asn	His	Tyr	2610	2615	2620
	Arg	Trp	Ile	Ile	Trp	Lys	Leu	Ala	Ala	Met	Glu	Cys	Ala	Phe	Pro	Lys	2625	2630	2635
	Glu	Phe	Ala	Asn	Arg	Cys	Leu	Ser	Pro	Glu	Arg	Val	Leu	Leu	Gln	Leu	2645	2650	2655
10	Lys	Tyr	Arg	Tyr	Asp	Thr	Glu	Ile	Asp	Arg	Ser	Arg	Arg	Ser	Ala	Ile	2660	2665	2670
	Lys	Lys	Ile	Met	Glu	Arg	Asp	Asp	Thr	Ala	Ala	Lys	Thr	Leu	Val	Leu	2675	2680	2685
15	Cys	Val	Ser	Asp	Ile	Ile	Ser	Leu	Ser	Ala	Asn	Ile	Ser	Glu	Thr	Ser	2690	2695	2700
	Ser	Asn	Lys	Thr	Ser	Ser	Ala	Asp	Thr	Gln	Lys	Val	Ala	Ile	Ile	Glu	2705	2710	2715
	Leu	Thr	Asp	Gly	Trp	Tyr	Ala	Val	Lys	Ala	Gln	Leu	Asp	Pro	Pro	Leu	2725	2730	2735
20	Leu	Ala	Val	Leu	Lys	Asn	Gly	Arg	Leu	Thr	Val	Gly	Gln	Lys	Ile	Ile	2740	2745	2750
	Leu	His	Gly	Ala	Glu	Leu	Val	Gly	Ser	Pro	Asp	Ala	Cys	Thr	Pro	Leu	2755	2760	2765
25	Glu	Ala	Pro	Glu	Ser	Leu	Met	Leu	Lys	Ile	Ser	Ala	Asn	Ser	Thr	Arg	2770	2775	2780
	Pro	Ala	Arg	Trp	Tyr	Thr	Lys	Leu	Gly	Phe	Phe	Pro	Asp	Pro	Arg	Pro	2785	2790	2795
	Phe	Pro	Leu	Pro	Leu	Ser	Ser	Leu	Phe	Ser	Asp	Gly	Gly	Asn	Val	Gly	2805	2810	2815
30	Cys	Val	Asp	Val	Ile	Ile	Gln	Arg	Ala	Tyr	Pro	Ile	Gln	Trp	Met	Glu	2820	2825	2830
	Lys	Thr	Ser	Ser	Gly	Leu	Tyr	Ile	Phe	Arg	Asn	Glu	Arg	Glu	Glu	Glu	2835	2840	2845
35	Lys	Glu	Ala	Ala	Lys	Tyr	Val	Glu	Ala	Gln	Gln	Lys	Arg	Leu	Glu	Ala	2850	2855	2860
	Leu	Phe	Thr	Lys	Ile	Gln	Glu	Glu	Phe	Glu	Glu	His	Glu	Glu	Asn	Thr	2865	2870	2875
	Thr	Lys	Pro	Tyr	Leu	Pro	Ser	Arg	Ala	Leu	Thr	Arg	Gln	Gln	Val	Arg	2885	2890	2895
40	Ala	Leu	Gln	Asp	Gly	Ala	Glu	Leu	Tyr	Glu	Ala	Val	Lys	Asn	Ala	Ala	2900	2905	2910
	Asp	Pro	Ala	Tyr	Leu	Glu	Gly	Tyr	Phe	Ser	Glu	Glu	Gln	Leu	Arg	Ala	2915	2920	2925
45	Leu	Asn	Asn	His	Arg	Gln	Met	Leu	Asn	Asp	Lys	Lys	Gln	Ala	Gln	Ile	2930	2935	2940
	Gln	Leu	Glu	Ile	Arg	Lys	Ala	Met	Glu	Ser	Ala	Glu	Gln	Lys	Glu	Gln	2945	2950	2955
	Gly	Leu	Ser	Arg	Asp	Val	Thr	Thr	Val	Trp	Lys	Leu	Arg	Ile	Val	Ser	2965	2970	2975
50	Tyr	Ser	Lys	Lys	Glu	Lys	Asp	Ser	Val	Ile	Leu	Ser	Ile	Trp	Arg	Pro	2980	2985	2990
	Ser	Ser	Asp	Leu	Tyr	Ser	Leu	Leu	Thr	Glu	Gly	Lys	Arg	Tyr	Arg	Ile	2995	3000	3005
	Tyr	His	Leu	Ala	Thr	Ser	Lys	Ser	Lys	Ser	Lys	Ser	Glu	Arg	Ala	Asn	3010	3015	3020
55	Ile	Gln	Leu	Ala	Ala	Thr	Lys	Lys	Thr	Gln	Tyr	Gln	Gln	Leu	Pro	Val	3025	3030	3035
	Ser	Asp	Glu	Ile	Leu	Phe	Gln	Ile	Tyr	Gln	Pro	Arg	Glu	Pro	Leu	His	3045	3050	3055
60	Phe	Ser	Lys	Phe	Leu	Asp	Pro	Asp	Phe	Gln	Pro	Ser	Cys	Ser	Glu	Val	3060	3065	3070
	Asp	Leu	Ile	Gly	Phe	Val	Val	Ser	Val	Val	Lys	Lys	Thr	Gly	Leu	Ala			

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	GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC	60
	TCTGCTGCGC CTCGGGTGTC TTTTGC GCGC GTGGGTGCGC GCCGGGAGAA GCGTGAGGGG	120
	ACAGATTTGT GACCGGCGCG GTTTTGTCA GCTTACTCCG GCCAAAAAG AACTGCACCT	180
5	CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT	237
	Met Pro Ile	
	1	
10	GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC	285
	Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys	
	5 10 15	
	AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT	333
	Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu	
15	20 25 30 35	
	TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA	381
	Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	
	40 45 50	
	CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG	429
	His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	
	55 60 65	
25	AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG	477
	Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu	
	70 75 80	
30	CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT	525
	Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp	
	85 90 95	
	AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA	573
	Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys	
35	100 105 110 115	
	AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC	621
	Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser	
	120 125 130	
40	TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA	669
	Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	
	135 140 145	
45	TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT	717
	Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	
	150 155 160	
50	TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT	765
	Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	
	165 170 175	
55	ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA	813
	Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	
	180 185 190 195	
	AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC	861
	Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	
	200 205 210	
60	AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT	909
	Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	

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10
Sub
15
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	215	220	225	
5	AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn 230 235 240			957
	GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg 245 250 255			1005
	GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys 260 265 270 275			1053
	GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA CAT GTC CTA Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro His Val Leu 280 285 290			1101
20	GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser 295 300 305			1149
25	TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val 310 315 320			1197
30	AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp 325 330 335			1245
	GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val 340 345 350 355			1293
35	TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala 360 365 370			1341
40	CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val 375 380 385			1389
45	GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu 390 395 400			1437
50	AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys 405 410 415			1485
	GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg 420 425 430 435			1533
55	AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser 440 445 450			1581
60	OTA CCA AAA TCG GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys 455 460 465			1629

5 AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA 1677
 Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala
 470 475 480

10 GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG 1725
 Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln
 485 490 495

15 GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT 1773
 Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr
 500 505 510 515

20 TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA 1821
 Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys
 520 525 530

25 GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA 1869
 Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser
 535 540 545

30 CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG 1917
 Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp
 550 555 560

35 CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA 1965
 Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu
 565 570 575

40 ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT 2013
 Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His
 580 585 590 595

45 GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA 2061
 Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser
 600 605 610

50 GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA 2109
 Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala
 615 620 625

55 CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG 2157
 Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val
 630 635 640

60 AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA 2205
 Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu
 645 650 655

65 ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA 2253
 Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr
 660 665 670 675

70 TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA 2301
 Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala
 680 685 690

75 AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT 2349
 Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp
 695 700 705

	TCT	CTG	TCA	TGC	CTG	CAG	GAA	GGA	CAG	TGT	GAA	AAT	GAT	CCA	AAA	AGC	2397
	Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp	Pro	Lys	Ser	
			710					715					720				
5	AAA	AAA	GTT	TCA	GAT	ATA	AAA	GAA	GAG	GTC	TTG	GCT	GCA	GCA	TGT	CAC	2445
	Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala	Ala	Cys	His	
			725					730					735				
10	CCA	GTA	CAA	CAC	TCA	AAA	GTG	GAA	TAC	AGT	GAT	ACT	GAC	TTT	CAA	TCC	2493
	Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp	Phe	Gln	Ser	
			740					745					750			755	
15	CAG	AAA	AGT	CTT	TTA	TAT	GAT	CAT	GAA	AAT	GCC	AGC	ACT	CTT	ATT	TTA	2541
	Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr	Leu	Ile	Leu	
					760						765				770		
20	ACT	CCT	ACT	TCC	AAG	GAT	GTT	CTG	TCA	AAC	CTA	GTC	ATG	ATT	TCT	AGA	2589
	Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met	Ile	Ser	Arg	
				775					780						785		
25	GGC	AAA	GAA	TCA	TAC	AAA	ATG	TCA	GAC	AAG	CTC	AAA	GGT	AAC	AAT	TAT	2637
	Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly	Asn	Asn	Tyr	
			790						795				800				
30	GAA	TCT	GAT	GTT	GAA	TTA	ACC	AAA	AAT	ATT	CCC	ATG	GAA	AAG	AAT	CAA	2685
	Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu	Lys	Asn	Gln	
			805					810					815				
35	GAT	GTA	TGT	GCT	TTA	AAT	GAA	AAT	TAT	AAA	AAC	GTT	GAG	CTG	TTG	CCA	2733
	Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu	Leu	Leu	Pro	
			820				825					830				835	
40	CCT	GAA	AAA	TAC	ATG	AGA	GTA	GCA	TCA	CCT	TCA	AGA	AAG	GTA	CAA	TTC	2781
	Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys	Val	Gln	Phe	
					840						845				850		
45	AAC	CAA	AAC	ACA	AAT	CTA	AGA	GTA	ATC	CAA	AAA	AAT	CAA	GAA	GAA	ACT	2829
	Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln	Glu	Glu	Thr	
				855					860					865			
50	ACT	TCA	ATT	TCA	AAA	ATA	ACT	GTC	AAT	CCA	GAC	TCT	GAA	GAA	CTT	TTC	2877
	Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu	Glu	Leu	Phe	
			870						875				880				
55	TCA	GAC	AAT	GAG	AAT	AAT	TTT	GTC	TTC	CAA	ATA	GCT	AAT	GAA	AGG	AAT	2925
	Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Ile	Ala	Asn	Glu	Arg	Asn	
			885					890					895				
60	AAT	CTT	GCT	TTA	GGA	AAT	ACT	AAG	GAA	CTT	CAT	GAA	ACA	GAC	TTG	ACT	2973
	Asn	Leu	Ala	Leu	Gly	Asn	Thr	Lys	Glu								

	Val	Tyr	Val	Leu	Ala	Glu	Glu	Asn	Lys	Asn	Ser	Val	Lys	Gln	His	Ile	
			950					955					960				
5	AAA	ATG	ACT	CTA	GGT	CAA	GAT	TTA	AAA	TCG	GAC	ATC	TCC	TTG	AAT	ATA	3165
	Lys	Met	Thr	Leu	Gly	Gln	Asp	Leu	Lys	Ser	Asp	Ile	Ser	Leu	Asn	Ile	
		965					970					975					
10	GAT	AAA	ATA	CCA	GAA	AAA	AAT	AAT	GAT	TAC	ATG	GAC	AAA	TGG	GCA	GGA	3213
	Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met	Asp	Lys	Trp	Ala	Gly	
		980				985					990					995	
15	CTC	TTA	GGT	CCA	ATT	TCA	AAT	CAC	AGT	TTT	GGA	GGT	AGC	TTC	AGA	ACA	3261
	Leu	Leu	Gly	Pro	Ile	Ser	Asn	His	Ser	Phe	Gly	Gly	Ser	Phe	Arg	Thr	
				1000						1005					1010		
20	GCT	TCA	AAT	AAG	GAA	ATC	AAG	CTC	TCT	GAA	CAT	AAC	ATT	AAG	AAG	AGC	3309
	Ala	Ser	Asn	Lys	Glu	Ile	Lys	Leu	Ser	Glu	His	Asn	Ile	Lys	Lys	Ser	
			1015					1020						1025			
25	AAA	ATG	TTC	TTC	AAA	GAT	ATT	GAA	GAA	CAA	TAT	CCT	ACT	AGT	TTA	GCT	3357
	Lys	Met	Phe	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr	Pro	Thr	Ser	Leu	Ala	
			1030				1035						1040				
30	TGT	GTT	GAA	ATT	GTA	AAT	ACC	TTG	GCA	TTA	GAT	AAT	CAA	AAG	AAA	CTG	3405
	Cys	Val	Glu	Ile	Val	Asn	Thr	Leu	Ala	Leu	Asp	Asn	Gln	Lys	Lys	Leu	
		1045				1050						1055					
35	AGC	AAG	CCT	CAG	TCA	ATT	AAT	ACT	GTA	TCT	GCA	CAT	TTA	CAG	AGT	AGT	3453
	Ser	Lys	Pro	Gln	Ser	Ile	Asn	Thr	Val	Ser	Ala	His	Leu	Gln	Ser	Ser	
		1060				1065					1070				1075		
40	GTA	GTT	GTT	TCT	GAT	TGT	AAA	AAT	AGT	CAT	ATA	ACC	CCT	CAG	ATG	TTA	3501
	Val	Val	Val	Ser	Asp	Cys	Lys	Asn	Ser	His	Ile	Thr	Pro	Gln	Met	Leu	
				1080						1085					1090		
45	TTT	TCC	AAG	CAG	GAT	TTT	AAT	TCA	AAC	CAT	AAT	TTA	ACA	CCT	AGC	CAA	3549
	Phe	Ser	Lys	Gln	Asp	Phe	Asn	Ser	Asn	His	Asn	Leu	Thr	Pro	Ser	Gln	
			1095					1100						1105			
50	AAG	GCA	GAA	ATT	ACA	GAA	CTT	TCT	ACT	ATA	TTA	GAA	GAA	TCA	GGA	AGT	3597
	Lys	Ala	Glu	Ile	Thr	Glu	Leu	Ser	Thr	Ile	Leu	Glu	Glu	Ser	Gly	Ser	
			1110				1115						1120				
55	CAG	TTT	GAA	TTT	ACT	CAG	TTT	AGA	AAA	CCA	AGC	TAC	ATA	TTG	CAG	AAG	3645
	Gln	Phe	Glu	Phe	Thr	Gln	Phe	Arg	Lys	Pro	Ser	Tyr	Ile	Leu	Gln	Lys	
		1125				1130					1135						
60	AGT	ACA	TTT	GAA	GTG	CCT	GAA	AAC	CAG	ATG	ACT	ATC	TTA	AAG	ACC	ACT	3693
	Ser	Thr	Phe	Glu	Val	Pro	Glu	Asn	Gln	Met	Thr	Ile	Leu	Lys	Thr	Thr	
		1140				1145					1150				1155		
65	TCT	GAG	GAA	TGC	AGA	GAT	GCT	GAT	CTT	CAT	GTC	ATA	ATG	AAT	GCC	CCA	3741
	Ser	Glu	Glu	Cys	Arg	Asp	Ala	Asp	Leu	His	Val	Ile	Met	Asn	Ala	Pro	
				1160					1165					1170			
70	TCG	ATT	GGT	CAG	GTA	GAC	AGC	AGC	AAG	CAA	TTT	GAA	GGT	ACA	GTT	GAA	3789
	Ser	Ile	Gly	Gln	Val	Asp	Ser	Ser	Lys	Gln	Phe	Glu	Gly	Thr	Val	Glu	
			1175						1180					1185			
75	ATT	AAA	CGG	AAG	TTT	GCT	GGC	CTG	TTG	AAA	AAT	GAC	TGT	AAC	AAA	AGT	3837
	Ile	Lys	Arg	Lys	Phe	Ala	Gly	Leu	Leu	Lys	Asn	Asp	Cys	Asn	Lys	Ser	

1190

1195

1200

5 GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT 3885
Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe
1205 1210 1215

10 TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA 3933
Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln
1220 1225 1230 1235

AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT 3981
Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr
1240 1245 1250

15 TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT 4029
Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp
1255 1260 1265

20 TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA 4077
Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val
1270 1275 1280

25 AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA 4125
Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu
1285 1290 1295

30 ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA 4173
Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg
1300 1305 1310 1315

AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT 4221
Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser
1320 1325 1330

35 CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT 4269
His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val
1335 1340 1345

40 TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC 4317
Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn
1350 1355 1360

45 ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG 4365
Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln
1365 1370 1375

50 ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT 4413
Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala
1380 1385 1390 1395

CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT 4461
Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala
1400 1405 1410

55 ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT 4509
Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe
1415 1420 1425

60 TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT 4557
Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe
1430 1435 1440

0004471 05559

5 AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC 4605
Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn
1445 1450 1455

10 TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG 4653
Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met
1460 1465 1470 1475

15 GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG 4701
Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu
1480 1485 1490

20 AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG 4749
Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln
1495 1500 1505

25 GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA COT ACT CTG TTG GGT 4797
Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly
1510 1515 1520

30 TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG 4845
Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu
1525 1530 1535

35 GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA 4893
Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu
1540 1545 1550 1555

40 ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG 4941
Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu
1560 1565 1570

45 GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT 4989
Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala
1575 1580 1585

50 GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC 5037
Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn
1590 1595 1600

55 CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT 5085
Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn
1605 1610 1615

60 TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG 5133
Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu
1620 1625 1630 1635

AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT 5181
Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro
1640 1645 1650

GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA 5229
Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser
1655 1660 1665

GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG 5277
Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln
1670 1675 1680

5 ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT 5325
 Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp
 1685 1690 1695

10 GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG 5373
 Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu
 1700 1705 1710 1715

15 TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT 5421
 Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His
 1720 1725 1730

20 CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC 5469
 Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn
 1735 1740 1745

25 AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC 5517
 Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu
 1750 1755 1760

30 TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT 5565
 Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val
 1765 1770 1775

35 GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA 5613
 Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys
 1780 1785 1790 1795

40 GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG 5661
 Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu
 1800 1805 1810

45 GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT 5709
 Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile
 1815 1820 1825

50 AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA 5757
 Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala
 1830 1835 1840

55 TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT 5805
 Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile
 1845 1850 1855

60 AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG 5853
 Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys
 1860 1865 1870 1875

65 GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA 5901
 Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala
 1880 1885 1890

70 GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT 5949
 Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser
 1895 1900 1905

75 CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC 5997
 Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp
 1910 1915 1920

80 ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG 6045

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Sub
A1

	Ile	Gln	Ser	Glu	Glu	Ile	Leu	Gln	His	Asn	Gln	Asn	Met	Ser	Gly	Leu	
	1925						1930				1935						
5	GAG	AAA	GTT	TCT	AAA	ATA	TCA	CCT	TGT	GAT	GTT	AGT	TTG	GAA	ACT	TCA	6093
	Glu	Lys	Val	Ser	Lys	Ile	Ser	Pro	Cys	Asp	Val	Ser	Leu	Glu	Thr	Ser	
	1940					1945					1950					1955	
	GAT	ATA	TGT	AAA	TGT	AGT	ATA	GGG	AAG	CTT	CAT	AAG	TCA	GTC	TCA	TCT	6141
10	Asp	Ile	Cys	Lys	Cys	Ser	Ile	Gly	Lys	Leu	His	Lys	Ser	Val	Ser	Ser	
					1960					1965						1970	
	GCA	AAT	ACT	TGT	GGG	ATT	TTT	AGC	ACA	GCA	AGT	GGA	AAA	TCT	GTC	CAG	6189
	Ala	Asn	Thr	Cys	Gly	Ile	Phe	Ser	Thr	Ala	Ser	Gly	Lys	Ser	Val	Gln	
15					1975				1980					1985			
	GTA	TCA	GAT	GCT	TCA	TTA	CAA	AAC	GCA	AGA	CAA	GTG	TTT	TCT	GAA	ATA	6237
	Val	Ser	Asp	Ala	Ser	Leu	Gln	Asn	Ala	Arg	Gln	Val	Phe	Ser	Glu	Ile	
			1990					1995					2000				
20	GAA	GAT	AGT	ACC	AAG	CAA	GTC	TTT	TCC	AAA	GTA	TTG	TTT	AAA	AGT	AAC	6285
	Glu	Asp	Ser	Thr	Lys	Gln	Val	Phe	Ser	Lys	Val	Leu	Phe	Lys	Ser	Asn	
			2005				2010					2015					
25	GAA	CAT	TCA	GAC	CAG	CTC	ACA	AGA	GAA	GAA	AAT	ACT	GCT	ATA	CGT	ACT	6333
	Glu	His	Ser	Asp	Gln	Leu	Thr	Arg	Glu	Glu	Asn	Thr	Ala	Ile	Arg	Thr	
	2020				2025						2030					2035	
	CCA	GAA	CAT	TTA	ATA	TCC	CAA	AAA	GGC	TTT	TCA	TAT	AAT	GTG	GTA	AAT	6381
30	Pro	Glu	His	Leu	Ile	Ser	Gln	Lys	Gly	Phe	Ser	Tyr	Asn	Val	Val	Asn	
					2040				2045						2050		
	TCA	TCT	GCT	TTC	TCT	GGA	TTT	AGT	ACA	GCA	AGT	GGA	AAG	CAA	GTT	TCC	6429
35	Ser	Ser	Ala	Phe	Ser	Gly	Phe	Ser	Thr	Ala	Ser	Gly	Lys	Gln	Val	Ser	
				2055				2060						2065			
	ATT	TTA	GAA	AGT	TCC	TTA	CAC	AAA	GTT	AAG	GGA	GTG	TTA	GAG	GAA	TTT	6477
	Ile	Leu	Glu	Ser	Ser	Leu	His	Lys	Val	Lys	Gly	Val	Leu	Glu	Glu	Phe	
			2070					2075					2080				
40	GAT	TTA	ATC	AGA	ACT	GAG	CAT	AGT	CTT	CAC	TAT	TCA	CCT	ACG	TCT	AGA	6525
	Asp	Leu	Ile	Arg	Thr	Glu	His	Ser	Leu	His	Tyr	Ser	Pro	Thr	Ser	Arg	
			2085				2090					2095					
45	CAA	AAT	GTA	TCA	AAA	ATA	CTT	CCT	CGT	GTT	GAT	AAG	AGA	AAC	CCA	GAG	6573
	Gln	Asn	Val	Ser	Lys	Ile	Leu	Pro	Arg	Val	Asp	Lys	Arg	Asn	Pro	Glu	
	2100					2105					2110				2115		
	CAC	TGT	GTA	AAC	TCA	GAA	ATG	GAA	AAA	ACC	TGC	AGT	AAA	GAA	TTT	AAA	6621
50	His	Cys	Val	Asn	Ser	Glu	Met	Glu	Lys	Thr	Cys	Ser	Lys	Glu	Phe	Lys	
					2120					2125					2130		
	TTA	TCA	AAT	AAC	TTA	AAT	GTT	GAA	GGT	GGT	TCT	TCA	GAA	AAT	AAT	CAC	6669
	Leu	Ser	Asn	Asn	Leu	Asn	Val	Glu	Gly	Gly	Ser	Ser	Glu	Asn	Asn	His	
55					2135				2140					2145			
	TCT	ATT	AAA	GTT	TCT	CCA	TAT	CTC	TCT	CAA	TTT	CAA	CAA	GAC	AAA	CAA	6717
	Ser	Ile	Lys	Val	Ser	Pro	Tyr	Leu	Ser	Gln	Phe	Gln	Gln	Asp	Lys	Gln	
			2150					2155					2160				
60	CAG	TTG	GTA	TTA	GGA	ACC	AAA	GTC	TCA	CTT	GTT	GAG	AAC	ATT	CAT	GTT	6765
	Gln	Leu	Val	Leu	Gly	Thr	Lys	Val	Ser	Leu	Val	Glu	Asn	Ile	His	Val	

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2165	2170	2175	
TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly 2180 2185 2190 2195			6813
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val 2200 2205 2210			6861
TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala 2215 2220 2225			6909
GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser 2230 2235 2240			6957
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn 2245 2250 2255			7005
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu 2260 2265 2270 2275			7053
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn 2280 2285 2290			7101
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser 2295 2300 2305			7149
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His 2310 2315 2320			7197
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys 2325 2330 2335			7245
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu 2340 2345 2350 2355			7293
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser 2360 2365 2370			7341
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala 2375 2380 2385			7389
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr 2390 2395 2400			7437
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val 2405 2410 2415			7485

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	GAA	CAG	TGT	GTT	AGG	AAT	ATT	AAC	TTG	GAG	GAA	AAC	AGA	CAA	AAG	CAA	
	Glu	Gln	Cys	Val	Arg	Asn	Ile	Asn	Leu	Glu	Glu	Asn	Arg	Gln	Lys	Gln	
5	2420					2425				2430					2435		7533
	AAC	ATT	GAT	GGA	CAT	GGC	TCT	GAT	GAT	AGT	AAA	AAT	AAG	ATT	AAT	GAC	7581
	Asn	Ile	Asp	Gly	His	Gly	Ser	Asp	Asp	Ser	Lys	Asn	Lys	Ile	Asn	Asp	
				2440					2445						2450		
10	AAT	GAG	ATT	CAT	CAG	TTT	AAC	AAA	AAC	AAC	TCC	AAT	CAA	GCA	GCA	GCT	7629
	Asn	Glu	Ile	His	Gln	Phe	Asn	Lys	Asn	Asn	Ser	Asn	Gln	Ala	Ala	Ala	
				2455					2460					2465			
15	GTA	ACT	TTC	ACA	AAG	TGT	GAA	GAA	GAA	CCT	TTA	GAT	TTA	ATT	ACA	AGT	7677
	Val	Thr	Phe	Thr	Lys	Cys	Glu	Glu	Glu	Pro	Leu	Asp	Leu	Ile	Thr	Ser	
				2470					2475					2480			
20	CTT	CAG	AAT	GCC	AGA	GAT	ATA	CAG	GAT	ATG	CGA	ATT	AAG	AAG	AAA	CAA	7725
	Leu	Gln	Asn	Ala	Arg	Asp	Ile	Gln	Asp	Met	Arg	Ile	Lys	Lys	Lys	Gln	
				2485				2490						2495			
25	AGG	CAA	CGC	GTC	TTT	CCA	CAG	CCA	GGC	AGT	CTG	TAT	CTT	GCA	AAA	ACA	7773
	Arg	Gln	Arg	Val	Phe	Pro	Gln	Pro	Gly	Ser	Leu	Tyr	Leu	Ala	Lys	Thr	
	2500					2505					2510					2515	
30	TCC	ACT	CTG	CCT	CGA	ATC	TCT	CTG	AAA	GCA	GCA	GTA	GGA	GGC	CAA	GTT	7821
	Ser	Thr	Leu	Pro	Arg	Ile	Ser	Leu	Lys	Ala	Ala	Val	Gly	Gly	Gln	Val	
				2520						2525					2530		
35	CCC	TCT	GCG	TGT	TCT	CAT	AAA	CAG	CTG	TAT	ACG	TAT	GGC	GTT	TCT	AAA	7869
	Pro	Ser	Ala	Cys	Ser	His	Lys	Gln	Leu	Tyr	Thr	Tyr	Gly	Val	Ser	Lys	
				2535					2540					2545			
40	CAT	TGC	ATA	AAA	ATT	AAC	AGC	AAA	AAT	GCA	GAG	TCT	TTT	CAG	TTT	CAC	7917
	His	Cys	Ile	Lys	Ile	Asn	Ser	Lys	Asn	Ala	Glu	Ser	Phe	Gln	Phe	His	
				2550				2555						2560			
45	ACT	GAA	GAT	TAT	TTT	GGT	AAG	GAA	AGT	TTA	TGG	ACT	GGA	AAA	GGA	ATA	7965
	Thr	Glu	Asp	Tyr	Phe	Gly	Lys	Glu	Ser	Leu	Trp	Thr	Gly	Lys	Gly	Ile	
				2565				2570					2575				
50	CAG	TTG	GCT	GAT	GGT	GGA	TGG	CTC	ATA	CCC	TCC	AAT	GAT	GGA	AAG	GCT	8013
	Gln	Leu	Ala	Asp	Gly	Gly	Trp	Leu	Ile	Pro	Ser	Asn	Asp	Gly	Lys	Ala	
	2580					2585					2590					2595	
55	GGA	AAA	GAA	GAA	TTT	TAT	AGG	GCT	CTG	TGT	GAC	ACT	CCA	GGT	GTG	GAT	8061
	Gly	Lys	Glu	Glu	Phe	Tyr	Arg	Ala	Leu	Cys	Asp	Thr	Pro	Gly	Val	Asp	
				2600					2605						2610		
60	CCA	AAG	CTT	ATT	TCT	AGA	ATT	TGG	GTT	TAT	AAT	CAC	TAT	AGA	TGG	ATC	8109

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	TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA	8253
	Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile	
	2660 2665 2670 2675	
5	ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT	8301
	Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser	
	2680 2685 2690	
10	GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA	8349
	Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys	
	2695 2700 2705	
15	ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT	8397
	Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp	
	2710 2715 2720	
20	GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC	8445
	Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val	
	2725 2730 2735	
25	TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA	8493
	Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly	
	2740 2745 2750 2755	
30	GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA	8541
	Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro	
	2760 2765 2770	
35	GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC	8589
	Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg	
	2775 2780 2785	
40	TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG	8637
	Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu	
	2790 2795 2800	
45	CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT	8685
	Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp	
	2805 2810 2815	
50	GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA	8733
	Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser	
	2820 2825 2830 2835	
55	TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA	8781
	Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala	
	2840 2845 2850	
60	GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT	8829
	Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr	
	2855 2860 2865	
65	AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA	8877
	Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro	
	2870 2875 2880	
70	TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA	8925
	Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln	
	2885 2890 2895	
75	GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT	8973

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	3140		3145		3150		3155	
5	CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA							9741
	Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile							
		3160			3165		3170	
	CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT							9789
	Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn							
		3175			3180		3185	
	GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC							9837
	Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr							
		3190			3195		3200	
	ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT							9885
	Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser							
		3205			3210		3215	
20	CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC							9933
	Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala							
		3220			3225		3230	3235
	AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG							9981
25	Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys							
		3240			3245		3250	
	TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG							10029
	Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys							
30		3255			3260		3265	
	AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT							10077
	Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Val							
		3270			3275		3280	
35	AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG							10125
	Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln							
		3285			3290		3295	
40	CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA							10173
	Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys							
		3300			3305		3310	3315
	GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT							10221
45	Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile							
		3320			3325		3330	
	TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA							10269
	Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile							
50		3335			3340		3345	
	AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA							10317
	Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile							
		3350			3355		3360	
55	TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT							10365
	Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr							
		3365			3370		3375	
60	CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG							10413
	Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu							
		3380			3385		3390	3395

AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461
 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr
 5 3400 3405 3410

ATT ACA ACT AAA AAA TAT ATC TAA 10485
 Ile Thr Thr Lys Lys Tyr Ile
 3415

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3418 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

25 Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys
 1 5 10 15
 Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe
 20 25 30
 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu
 35 40 45
 Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
 50 55 60
 Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
 65 70 75 80
 35 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
 85 90 95
 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
 100 105 110
 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
 115 120 125
 40 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
 130 135 140
 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
 145 150 155 160
 45 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
 165 170 175
 Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
 180 185 190
 Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
 195 200 205
 50 Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
 210 215 220
 Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
 225 230 235 240
 55 Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
 245 250 255
 Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
 260 265 270
 Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
 275 280 285
 60 His Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
 290 295 300

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	785		790		795		800
	Asn Asn Tyr Glu Ser	Asp Val Glu Leu Thr	Lys Asn Ile Pro Met	Glu			
		805		810			815
5	Lys Asn Gln Asp Val	Cys Ala Leu Asn Glu	Asn Tyr Lys Asn Val	Glu			
		820		825			830
	Leu Leu Pro Pro Glu	Lys Tyr Met Arg Val	Ala Ser Pro Ser Arg	Lys			
		835		840			845
	Val Gln Phe Asn Gln	Asn Thr Asn Leu Arg	Val Ile Gln Lys Asn	Gln			
		850		855			860
	Glu Glu Thr Thr Ser	Ile Ser Lys Ile Thr	Val Asn Pro Asp Ser	Glu			
		865		870			880
	Glu Leu Phe Ser Asp	Asn Glu Asn Asn Phe	Val Phe Gln Ile Ala	Asn			
		885		890			895
15	Glu Arg Asn Asn Leu	Ala Leu Gly Asn Thr	Lys Glu Leu His Glu	Thr			
		900		905			910
	Asp Leu Thr Cys Val	Asn Glu Pro Ile Phe	Lys Asn Ser Thr Met	Val			
		915		920			925
	Leu Tyr Gly Asp Thr	Gly Asp Lys Gln Ala	Thr Gln Val Ser Ile	Lys			
		930		935			940
	Lys Asp Leu Val Tyr	Val Leu Ala Glu Glu	Asn Lys Asn Ser Val	Lys			
		945		950			955
	Gln His Ile Lys Met	Thr Leu Gly Gln Asp	Leu Lys Ser Asp Ile	Ser			
		965		970			975
25	Leu Asn Ile Asp Lys	Ile Pro Glu Lys Asn	Asn Asp Tyr Met Asp	Lys			
		980		985			990
	Trp Ala Gly Leu Leu	Gly Pro Ile Ser Asn	His Ser Phe Gly Gly	Ser			
		995		1000			1005
	Phe Arg Thr Ala Ser	Asn Lys Glu Ile Lys	Leu Ser Glu His Asn	Ile			
		1010		1015			1020
30	Lys Lys Ser Lys Met	Phe Phe Lys Asp Ile	Glu Glu Gln Tyr Pro	Thr			
		1025		1030			1035
	Ser Leu Ala Cys Val	Glu Ile Val Asn Thr	Leu Ala Leu Asp Asn	Gln			
		1045		1050			1055
35	Lys Lys Leu Ser Lys	Pro Gln Ser Ile Asn	Thr Val Ser Ala His	Leu			
		1060		1065			1070
	Gln Ser Ser Val Val	Val Ser Asp Cys Lys	Asn Ser His Ile Thr	Pro			
		1075		1080			1085
	Gln Met Leu Phe Ser	Lys Gln Asp Phe Asn	Ser Asn His Asn Leu	Thr			
		1090		1095			1100
40	Pro Ser Gln Lys Ala	Glu Ile Thr Glu Leu	Ser Thr Ile Leu Glu	Glu			
		1105		1110			1115
	Ser Gly Ser Gln Phe	Glu Phe Thr Gln Phe	Arg Lys Pro Ser Tyr	Ile			
		1125		1130			1135
45	Leu Gln Lys Ser Thr	Phe Glu Val Pro Glu	Asn Gln Met Thr Ile	Leu			
		1140		1145			1150
	Lys Thr Thr Ser Glu	Glu Cys Arg Asp Ala	Asp Leu His Val Ile	Met			
		1155		1160			1165
	Asn Ala Pro Ser Ile	Gly Gln Val Asp Ser	Ser Lys Gln Phe Glu	Gly			
		1170		1175			1180
50	Thr Val Glu Ile Lys	Arg Lys Phe Ala Gly	Leu Leu Lys Asn Asp	Cys			
		1185		1190			1195
	Asn Lys Ser Ala Ser	Gly Tyr Leu Thr Asp	Glu Asn Glu Val Gly	Phe			
		1205		1210			1215
55	Arg Gly Phe Tyr Ser	Ala His Gly Thr Lys	Leu Asn Val Ser Thr	Glu			
		1220		1225			1230
	Ala Leu Gln Lys Ala	Val Lys Leu Phe Ser	Asp Ile Glu Asn Ile	Ser			
		1235		1240			1245
	Glu Glu Thr Ser Ala	Glu Val His Pro Ile	Ser Leu Ser Ser Ser	Lys			
		1250		1255			1260
60	Cys His Asp Ser Val	Val Ser Met Phe Lys	Ile Glu Asn His Asn	Asp			
		1265		1270			1275
							128

Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
 1285 1290 1295
 5 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
 1300 1305 1310
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
 1315 1320 1325
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
 1330 1335 1340
 10 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
 1345 1350 1355 136
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
 1365 1370 1375
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
 1380 1385 1390
 15 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
 1395 1400 1405
 Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
 1410 1415 1420
 20 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
 1425 1430 1435 144
 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
 1445 1450 1455
 25 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
 1460 1465 1470
 Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
 1475 1480 1485
 Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
 1490 1495 1500
 30 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
 1505 1510 1515 152
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
 1525 1530 1535
 35 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
 1540 1545 1550
 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
 1555 1560 1565
 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
 1570 1575 1580
 40 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
 1585 1590 1595 160
 Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
 1605 1610 1615
 45 Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
 1620 1625 1630
 Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
 1635 1640 1645
 Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
 1650 1655 1660
 50 Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
 1665 1670 1675 168
 Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
 1685 1690 1695
 55 Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
 1700 1705 1710
 Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
 1715 1720 1725
 Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
 1730 1735 1740
 60 Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
 1745 1750 1755 176
 Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu

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	Pro	Glu	Asn	Glu	Glu	Met	Val	Leu	Ser	Asn	Ser	Arg	Ile	Gly	Lys	Arg
				2260					2265					2270		
5	Arg	Gly	Glu	Pro	Leu	Ile	Leu	Val	Gly	Glu	Pro	Ser	Ile	Lys	Arg	Asn
			2275					2280					2285			
	Leu	Leu	Asn	Glu	Phe	Asp	Arg	Ile	Ile	Glu	Asn	Gln	Glu	Lys	Ser	Leu
			2290				2295					2300				
	Lys	Ala	Ser	Lys	Ser	Thr	Pro	Asp	Gly	Thr	Ile	Lys	Asp	Arg	Arg	Leu
			2305				2310					2315				232
10	Phe	Met	His	His	Val	Ser	Leu	Glu	Pro	Ile	Thr	Cys	Val	Pro	Phe	Arg
				2325						2330					2335	
	Thr	Thr	Lys	Glu	Arg	Gln	Glu	Ile	Gln	Asn	Pro	Asn	Phe	Thr	Ala	Pro
				2340						2345				2350		
15	Gly	Gln	Glu	Phe	Leu	Ser	Lys	Ser	His	Leu	Tyr	Glu	His	Leu	Thr	Leu
			2355					2360				2365				
	Glu	Lys	Ser	Ser	Ser	Asn	Leu	Ala	Val	Ser	Gly	His	Pro	Phe	Tyr	Gln
			2370				2375					2380				
	Val	Ser	Ala	Thr	Arg	Asn	Glu	Lys	Met	Arg	His	Leu	Ile	Thr	Thr	Gly
			2385				2390				2395					240
20	Arg	Pro	Thr	Lys	Val	Phe	Val	Pro	Pro	Phe	Lys	Thr	Lys	Ser	His	Phe
				2405						2410					2415	
	His	Arg	Val	Glu	Gln	Cys	Val	Arg	Asn	Ile	Asn	Leu	Glu	Glu	Asn	Arg
				2420					2425					2430		
25	Gln	Lys	Gln	Asn	Ile	Asp	Gly	His	Gly	Ser	Asp	Asp	Ser	Lys	Asn	Lys
			2435					2440					2445			
	Ile	Asn	Asp	Asn	Glu	Ile	His	Gln	Phe	Asn	Lys	Asn	Asn	Ser	Asn	Gln
			2450				2455					2460				
	Ala	Ala	Ala	Val	Thr	Phe	Thr	Lys	Cys	Glu	Glu	Glu	Pro	Leu	Asp	Leu
			2465				2470					2475				248
30	Ile	Thr	Ser	Leu	Gln	Asn	Ala	Arg	Asp	Ile	Gln	Asp	Met	Arg	Ile	Lys
				2485						2490					2495	
	Lys	Lys	Gln	Arg	Gln	Arg	Val	Phe	Pro	Gln	Pro	Gly	Ser	Leu	Tyr	Leu
				2500					2505					2510		
	Ala	Lys	Thr	Ser	Thr	Leu	Pro	Arg	Ile	Ser	Leu	Lys	Ala	Ala	Val	Gly
35				2515				2520					2525			
	Gly	Gln	Val	Pro	Ser	Ala	Cys	Ser	His	Lys	Gln	Leu	Tyr	Thr	Tyr	Gly
			2530				2535					2540				
	Val	Ser	Lys	His	Cys	Ile	Lys	Ile	Asn	Ser	Lys	Asn	Ala	Glu	Ser	Phe
			2545				2550				2555					256
40	Gln	Phe	His	Thr	Glu	Asp	Tyr	Phe	Gly	Lys	Glu	Ser	Leu	Trp	Thr	Gly
				2565					2570						2575	
	Lys	Gly	Ile	Gln	Leu	Ala	Asp	Gly	Gly	Trp	Leu	Ile	Pro	Ser	Asn	Asp
				2580				2585					2590			
45	Gly	Lys	Ala	Gly	Lys	Glu	Glu	Phe	Tyr	Arg	Ala	Leu	Cys	Asp	Thr	Pro
			2595					2600					2605			
	Gly	Val	Asp	Pro	Lys	Leu	Ile	Ser	Arg	Ile	Trp	Val	Tyr	Asn	His	Tyr
			2610				2615					2620				
	Arg	Trp	Ile	Ile	Trp	Lys	Leu	Ala	Ala	Met	Glu	Cys	Ala	Phe	Pro	Lys
			2625				2630				2635					264
50	Glu	Phe	Ala	Asn	Arg	Cys	Leu	Ser	Pro	Glu	Arg	Val	Leu	Leu	Gln	Leu
				2645						2650					2655	
	Lys	Tyr	Arg	Tyr	Asp	Thr	Glu	Ile	Asp	Arg	Ser	Arg	Arg	Ser	Ala	Ile
				2660					2665					2670		
55	Lys	Lys	Ile	Met	Glu	Arg	Asp	Asp	Thr	Ala	Ala	Lys	Thr	Leu	Val	Leu
			2675					2680					2685			
	Cys	Val	Ser	Asp	Ile	Ile	Ser	Leu	Ser	Ala	Asn	Ile	Ser	Glu	Thr	Ser
			2690				2695					2700				
	Ser	Asn	Lys	Thr	Ser	Ser	Ala	Asp	Thr	Gln	Lys	Val	Ala	Ile	Ile	Glu
			2705				2710				2715					272
60	Leu	Thr	Asp	Gly	Trp	Tyr	Ala	Val	Lys	Ala	Gln	Leu	Asp	Pro	Pro	Leu
				2725						2730					2735	
	Leu	Ala	Val	Leu	Lys	Asn	Gly	Arg	Leu	Thr	Val	Gly	Gln	Lys	Ile	Ile

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(i) SEQUENCE CHARACTERISTICS:

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 2F primer

20

(i) /SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

41

(i) SEQUENCE CHARACTERISTICS:

158

(D) TOPOLOGY: linear

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- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: 3FII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GATCTTTAAC TGTTCTGGGT CACA

24

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: 3R1I primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCAGCATGA CACAATTAAT GA

22

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: 4F/M 13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGTAAAACGA CGGCCAGTAG AATGCAAATT TATAATCCAG AGTA

44

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: 4R-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCAGATTCA TCTTTATAGA AC

22

(2) INFORMATION FOR SEQ ID NO:21:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 5+6F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGTAAAACGA CGGCCAGTTG TGTGGCATT TTAAACATCA

40

20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 5+6R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CAGGAAACAG CTATGACCCA GGGCAAAGGT ATAACGCT

38

35

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 7F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGTAAAACGA CGGCCAGTTA AGTGAAATAA AGAGTGAA

38

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(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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- (A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 7R/M13R primer

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CAGGAAACAG CTATGACCAG AAGTATTAGA GATGAC

36

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 8F/M13F primer

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

25 TGTAACACGA CGGCCAGTGC CATATCTTAC CACCTTGTGA

40

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 8FIA primer

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTGCATTCTA GTGATAATAT AC

22

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 8RIA primer

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

60 AATTGTTAGC AATTTCAAC

19

(2) INFORMATION FOR SEQ ID NO:28:

000447.05299

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 9F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TGTAAAACGA CGGCCAGTTG GACCTAGGTT GATTGCAGAT

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 9R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGGAAACAG CTATGACCTA AACTGAGATC ACGGGTGACA

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 10AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAATAATATA AATTATATGG CTTA

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 10AR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAGGAAACAG CTATGACCCC TAGTCTTGCT AGTTCTT

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 10BF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGTAAAACGA CGGCCAGTAR CTGAAGTGGA ACCAAATGAT AC

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 10BR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAGGAAACAG CTATGACCAC GTGGCAAAGA ATTCTCTGAA GTAA

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 10CF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TGTAAAACGA CGGCCAGTCA GCATCTTGAA TCTCATACAG

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 10CRII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGACAGAGGT ACCTGAATC

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11AF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TGTAAAACGA CGGCCAGTTG GTACTTTAAT TTTGTCACCTT

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11AR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAGGAAACAG CTATGACCTG CAGGCATGAC AGAGAAT

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11BF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAGAAGCAAA ATGTAATAAG GA

22

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11BR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CATTTAAAGC ACATACATCT TG

22

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11CF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TCTAGAGGCA AAGAATCATA C

21

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11CR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CAAGATTATT CCTTTCATTA GC

22

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11DF primer

AACCAAACA CAAATCTAAG AG

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11DR primer

(xi) SEQUENCE DESCRIPTION: / SEQ ID NO: 43:

GTCATTTTTA TATGCTGCTT TAC

(2) INFORMATION FOR/SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11EF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGTTTTATAT GGAGACACAG G

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11ER primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GTATTACAA TTTCAACACA AGC

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(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11FF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATCACAGTTT TGGAGGTAGC

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11FR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTGACTTCCT GATTCTTCTA A

21

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11GF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTCAGATGTT ATTTTCCAAG C

21

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11GR primer

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTGTTAAATA ACCAGAAGCA C

21

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11HF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGGTAGACAG CAGCAAGC

18

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: None

(B) LOCATION:

(D) OTHER INFORMATION: 11HR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTAATATCAG TTGGCATTTA TT

22

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11IF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGCAGAGGTA CATCCAATAA G

21

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11IR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GATCAGTAAA TAGCAAGTCC G

21

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11JF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TACTGAAAAT GAAGATAACA AAT

23

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11JR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ATTTTGTCTTCT TTCTTATGTC AG

22

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11KF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TGTAAAACGA CGGCCAGTCT ACTAAAACGG AGCAA

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11KR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11LF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CACAAAATAC TGAAAGAAAG TG

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11LR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGCACCACAG TCTCAATAG

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11MF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GCAAAGACCC TAAAGTACAG

20

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11MR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CATCAAATAT TCCTTCTCTA AG

22

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11NF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TGTAAAACGA CGGCCAGTGA AAATTCAGCC TTAGC

35

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11NR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CAGGAAACAG CTATGACCAT CAGAATGGTA GGAAT

35

5 (2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11OF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

10
15
20 GTACTATAGC TGAAAATGAC AA

22

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11OR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

30
35 ACCACTGGCT ATCCTAAATG

20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11PF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

40
45
50
55 TGAAGATATT TCGGTTGAGG

20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11PR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

10 GTCAGCAAAA ACCTTATGTG 20

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11QF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

25 ACGAAAATTA TGGCAGGTTG T 21

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11QR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

45 CTTGTCTTGC GTTTTGTAAAT G 21

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11RF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

60 GCTTCATAAG TCAGTCTCAT 20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11RR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TCAAATTCCT CTAACACTCC

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11SF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGTAAAACGA CGGCCAGTTA CAGCAAGTGG AAAGC

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 11SR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAGGAAACAG CTATGACCAA GTTTCAGTTT TACCAAT

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (A) NAME/KEY:

(B) LOCATION:
(D) OTHER INFORMATION: 11TF primer

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTTCTTCAGA AAATAATCAC TC

22

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11TR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTAAAAAGA GAATGTGTGG C

21

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11UF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TGTAAAACGA CGGCCAGTAC TTTTCTGAT GTTCCTGTG

39

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 11UR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CAGGAAACAG CTATGACCTA AAAATAGTGA TTGGCAACA

39

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

5

10

15

42

20

25

30

35

4 C

45

50

55

6 C

21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

5

AAACGAGACT TTTCTCATAC TGTATTAG

28

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 14F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

20

ACCATGTAGC AAATGAGGGT CT

22

(2) INFORMATION FOR SEQ ID NO:83:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 14AR primer

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GCTTTTGTCT GTTTTCCTCC AA

22

40

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 15-2F primer

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

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CCAGGGGTTG TGCTTTTAA A

21

(2) INFORMATION FOR SEQ ID NO:85:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 15FUT/M13-R primer

CAGGAAACAG CTATGACCAC TCTGTCATAA AAGCCATC

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 16AF primer

TTTGGTTTGT TATAATTGTT TTTA

(2) INFORMATION/ FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 16AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CCAAC TTTT/ AGTTCGAGAG

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 17F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TTCAGTATCA TCCTATGTG

[illegible]

10
15
AGAA

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

20

(2) INFORMATION FOR SEQ ID NO:90:

(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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39

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(A) LENGTH: 38/base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45

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38

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(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

60

- (A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 19F/M13F primer

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TGTAAAACGA CGGCCAGTAA GTGAATATTT TTAAGGCAGT T

41

10

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 19FUT/M13-R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

25

CAGGAAACAG CTATGACCAA GAGACCGAAA CTCATCTC

39

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

35

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 20F/M13F primer

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TGTAAAACGA CGGCCAGTCA CTGTGCCTGG CCTGATAC

38

(2) INFORMATION FOR SEQ ID NO:95:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 20R/M13R primer

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CAGGAAACAG CTATGACCAT GTTAAATTCA AAGTCTCTA

39

60

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 21F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TGTAAAACGA CGGCCAGTGG GTGTTTTATG CTTGGTTCT

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 21R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CAGGAAACAG CTATGACCCA TTCAACATA TTCCTTCTG

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 22F-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AACCACACCC TTAAGATGA

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 22R-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

5 GCATTAGTAG TGGATTTTGC

20

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 23FII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

15
20 TCACTTCCAT TGCATC

16

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 23RII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

35
40 TGCCAACTGG TAGCTOC

17

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 24 2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

55
60 TACAGTTAGC AGCGACAAAA

20

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 24R/M13R primer

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CAGGAAACAG CTATGACCAT TTGCCAACTG GTAGCTCC

38

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

20

(A) NAME/KEY:

(B) LOCATION:

25

(D) OTHER INFORMATION: 25F-7/23 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GCTTTCGCCA AATTCAGCTA

20

30

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

40

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 25R-7/23 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

45

TACCAAAATG TGTGGTGATG

20

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50

55

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 26-2F primer

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

AATCACTGAT ACTGGTTTTG

20

5

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 26-2R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TATACTTACA GGAGCCACAT

20

20

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 27AF-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTGTGTGTAA TATTTGCG

35

18

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: 27AR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CAGGAAACAG CTATGACGGC AAGTTCTTCG TCAGCTATTG

55

40

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

60

- (A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 27BF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

TGTAAAACGA CGGCCAGTGA ATTCTCCTCA GATGACTCCA

40

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (A) NAME/KEY:
(B) LOCATION:
(D) OTHER INFORMATION: 27BR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CAGGAAACAG CTATGACCTC TTTGCTCATT GTGCAACA

38